

FIGURE 1

CGGACCGTGGGTGCGAGGCGAAGGTGACCAGGGGACCGAGCATT CAGATCTGCTCGGTAGA
 CCTGGTGCACCACCACTTCAGCTTACCAAGGCCTCCCTGTTGAAGAATTCCATCACGAAGAATCA
 ATGGCTTAAACACCTAGCAGGGAATATGCCACAAAACAAGAATTGGGATCCGGCGTGGGA
 GAACTGGCCAAGAACTCAAAGAGGCAGCATGGAACCATCGATGGAAAAAATATTAAAATT
 GATCAGATGGGAAGATGGTTGCTGGAGGGCTGCTGTTGGACTGGAGCATTGTGCTA
 CTATGGCTGGGACTGTCTAATGAGATTGGAGCTATTGAAAAGGCTGTAATTGGCCTCAGT
 ATGTCAAGGATAGAATTCCACCTATATGTA CTTAGCAGGGAGTATTGGTTAACAGCT
 TTGTCGCCATAGCAATCAGCAGAACGCCCTGAGCCATGGTGAGCTGGAATGCTGGTACGATCAATAC
 GGTGACAATTGGTGTGACCTTGAGCCATGGTGAGCTGCTACATTCTGGTGTGATGGGT
 CATATGACCAGAGCCCAGGCCAAAGCATCTTGCTTGCTGCTACATTCTGGTGTGATGGGT
 GCAGTGGTGGCCTCTGACAATATTAGGGGCTCTCTCATCAGAGCTGCATGGTACAC
 AGCTGGCATTGTGGGAGGCCTCTCCACTGTGGCCATGTGTGCGCCAGTGAAAAGTTCTGA
 ACATGGGTGCACCCCTGGGAGTGGGCCTGGGTCTCGTCTTGTGTCCTCATTGGGATCTATG
 TTTCTCCACCTACCACCGTGGCTGGCACTCTTACTCAGTGGCAATGTACGGTGGATT
 AGTTCTTTCAGCATGTTCTCTGTATGATA CCCAGAAAGTAATCAAGCGTGCAGAAGTAT
 CACCAATGTATGGAGTTCAAAATATGATCCCATTACTCGATGCTGAGTATCTACATGGAT
 ACATTAATATATTATGCGAGTTGCAACTATGCTGGCAACTGGAGGCAACAGAAAGAAAT**TG**
AAGTGACTCAGCTCTGGCTCTGCTACATCAAATATCTGTTAACGGGCAGATATGC
 ATTAAATAGTTGTACAAGCAGCTTCGTTGAAGTTAGAAGATAAGAAACATGTCACTCATA
 TTTAAATGTTCCGGAATGTGATGCCCTAGGTCTGCCTTTCTGGAGAATAATGCAGT
 AATCCTCTCCAAATAAGCACACACATTTCATTCTCATGTTGAGTGTGATTAAATGTT
 TTGGTGAATGTGAAAACCTAAAGTTGTCATGAGAATGTAAGTCTTTCTACTTTAA
 TTAGTAGGTTCACTGAGTAACCTAGCAAACTGTGTTGCATATTGGAGT
 GCAGAATATTGTAATTAAATGTCATAAGTGAATTGGAGCTTGTAAGGGGACCAAGAGAGAAG
 GAGTCACCTGCAGTCTTGTGTTAAATACTTAGAAACTTAGCACTGTGTTATTGATTA
 GTGAGGAGCCAGTAAGAAACATCTGGTATTGGAAACAAGTGGTCATTGTTACATTCA
 GCTGAACCTAACAAACTGTTCATCCTGAAACAGGCACAGGTGATGCATTCTCCTGCTGTTG
 CTTCTCAGTGCTCTCTTCAATATAGATGTTGACTGTTGACTGTACAGAATGTTAAC
 ATACAGAGAATCCTGATGGAATTATATATGTTGTTACTTTGAATGTTACAAAGGAA
 ATAACCTTAAACTATTCTCAAGAGAAAATTCAAAGCATGAAATATGTTGCTTTCCAG
 AATACAAACAGTATACTCATG

FIGURE 2

MLAARLVCLRTLPSRVFHPAFTKASPVVKNSITKNQWLLTPSREYATKTRIGIRRGRTGQEL
KEAALEPSMEKIFKIDQMGRWFVAGGAAVGLGALCYYGLGLSNEIGAIEKAVIWPQYVKDRI
HSTYMYLAGSIGLTALSIAIAISRTPVLMNFMMRGSWТИGVTFAMVGAGMLVRSIPYDQSP
GPKHLAWLLHSGVMGAVVAPLTIЛGGPLLIRAAWYTAGIVGGLSTVAMCAPSEKFLNMGAPL
GVGLGLVFVSSLGSMFLPPTTVAGATLYSVAMYGGLVLFSMFLLYDTQKVIKRAEVSPMYGV
QKYDPINSMLSИYMDTLNIFMRVATMLATGGNRKK

FIGURE 3

GAAGGCTGCCTCGCTGGTCCGAATTGGTGGCGCACGTCCGCCGTCTCGCCTCTGCAT
 CGCGGCTCGCGGCTCACCTAGACACCTAACAGTCGCGGAGCCGGCGTCGTGAGGG
 GGTCGGCACGGGGAGTCGGCGGTCTGTGCATCTGGTACCTGTGGTCGAAG**ATGT**CGG
 ACATCGGAGACTGGTCAGGAGCATCCCAGCGATCACCGCCTATTGGTCGCCACCCTC
 GCCGTGCCCTGGTCGGCAAACCTGGCCTCATCAGCCCGCCTACCTCTTCTGGCCCCGA
 AGCCTTCTTATCGCTTCAGATTGGAGGCCAATCACTGCCACCTTATTTCCCTGTGG
 GTCCAGGAACTGGATTCTTATTTGGTCAATTATTTCTTATATCAGTATTCTACGCGA
 CTTGAAACAGGAGCTTTGATGGGAGGCCAGCAGACTATTATTATGCTCCTTTAACTG
 GATTGACATCGTATTACTGGCTAGCAATGGATATGCAGTTGCTGATGATTCCCTGATCA
 TGTCAGTAATTATGTCGGGCCAGCTGAACAGAGACATGATTGATTCATTTGGTTTGA
 ACACGATTAAAGGCCTGCTATTACCTGGGTATCCTGGATTCAACTATATCATCGGAGG
 CTCGGTAATCAATGAGCTATTGGAAATCTGGTTGGACATCTTATTTCCTAATGTTCA
 GATAACCAATGGACTTGGGAGGAAGAAATTCTACACACCTCAGTTTGTACCGCTGG
 CTGCCAGTAGGAGAGGAGGTATCAGGATTGGTGTGCCCTGCTAGCATGAGGCGAGC
 TGCTGATCAGAATGGCGAGGCAGGAGACACAACACTGGGCCAGGGCTTCGACTGGAGACC
 AG**TGA**AGGGCGGCCCTCGGCAGCCGCTCCTCAAGCCACATTCCCTCCAGTGCTGGGTG
 CACTAACAACTGCCTCTGGCTAACACTGTTGGACCTGACCCACACTGAATGTAGTCTTC
 AGTACGAGACAAAGTCTTAAATCCGAAGAAAAATATAAGTGTCCACAAGTTACGAT
 TCTCATTCAAGCTTACTGCTGTGAAGAACAAATATAAGTGTCCACAAGTTACGAT
 TACATTTTGGTGTCTCTCTCCCTTCCGTCGAATAATGGGTTTAGCGGGTCT
 AATCTGCTGGCATTGAGCTGGGCTGGGTACCAAAACCTCCAAAAGGACCTTATCTCTT
 TCTTGACACATGCCTCTCCCACCTTCCAACCCCCACATTGCAACTAGAAAAAGTG
 CCCATAAAATTGCTCTGCCCTGACAGGTTCTGTTATTGACTTTGCCAAGGCTGGTC
 ACAACAAATCATATTACGTTATTTCCTTGGTGGCAGAACTGTTACCAATAGGGGAG
 AAGACAGCCACGGATGAAGCGTTCTCAGCTTGGAAATTGCTTCGACTGACATCCGTTGTT
 AACCGTTGCCACTCTCAGATATTAAAGTACCAACTGAGTTCATGAGGGCCA
 CAGATTGGTATTAAATGAGATACGAGGGTTGGTGTGGGTGTTGTTCTGAGCTAAGTGA
 TCAAGACTGTAGTGGAGTTGCAGCTAACATGGTTAGGTTAAACCATGGGGATGCACCC
 TTTGCGTTCTATGTAGCTGGCTACAGGGAGATGCTCTTGTAGGGAGTAGTTGGTTGCTTTGTT
 TAGGAGGATCCAGATCATGTTGGCTACAGGGAGATGCTCTTGTAGGGTCTGGGAT
 ATTCCCATTCAATCTCATCTGGATATGTGTCATTGAGTAAGGAGAGACCCCTCAT
 CGCTATTAAATGTCATTGCTATCCCCGTTTTGGTCATGTTCAATTAAATTGT
 GAGGAAGGCGCAGCTCTGACGTAGATCATTAAAGCTAATGTAAGCACATCTA
 AGGGAAATAACATGATTAAAGGTGAAATGGCTTGAATCATTGGTTGAGGGTGTGTA
 TTTGAGTCATGAATGTACAAGCTCTGTAATCAGACCAGCTAAATACCCACACCTTTT
 TCGTAGGTGGCTTCTACAGAGCTGGCTCATACCAAAATAAGTTTGAGGCA
 TGGCTTTCACACAGTTATTATGACGTTATCTGAAAGCAGACTGTTAGGAGCAGT
 ATTGAGTGGCTGTCACACTTGAGGCAACTAAAAGGCTCAACAGTCTTGTGATCAGTTCTT
 TTCAGGAAACATTGTGCTAACAGTATGACTATTCTTCCCCACTCTAAACAGTGTGAT
 GTGTGTTATCCTAGGAAATGAGAGCTGGCAAAACAACACTCTCATTTGAATAGAGTTGTG
 TACTTCTCCATATTAAATTATGATAAAATAGGTGGGGAGAGTCTGAACCTTAACGTCA
 TGTTTGTGTTCATCTGTCAGGACAAATAAGTTACTGTAAGGTTAGGGCATTACT
 CCAATTATGTTGACGTACACTCATTGACAGGCGTGGAGACTCATTGTATGTATAAGAATA
 TTTCTGACAGTGAGTGACCCGGAGTCTCTGGTGTACCCCTTCTACAGTCAGCTGCCGAG
 CAGTCATTCTTCTAAAGGTTACAAGTATTAGAACCTTCAGGTCAGGGCAAAATGTT
 ATGAAGTTATTCCCTTAAACATGGTTAGGAAGCTGATGACGTTATTGATTTGTCTGGATT
 ATGTTTGTGAAATAATTACCAAAAGCTATTGAGTTTGACTGACAAAGGCAAAACA
 TGACAGTGGAATTCTCTTACAAATGGAAAAAAATCCTTATTGTATAAGGACTTCCC
 TTTTGTAACATCCTTTATTGGTAAAATTGTAACATGCAACTTG

FIGURE 4

MSDIGDWFRSIPAITRYWFAATVAVPLVGKILGLISPAYLFLWPEAFLYRFQIWRPITATFYF
PVGPGTGFYLVNLFLYQYSTRLETGAFDGRPADYLFMLLFNWICIVITGLAMDMQLLMIP
LIMSVLYVWAQLNRDMIVSFWFGTRFKACYILPWVILGFNYIIGGSVINELIGNLVGHLYFFL
MFRYPMDLGGRNFLSTPQFLYRWLPSRRGGVSGFGVPPASMRRAADQNGGGGRHNWGQGFRL
GDQ

Transmembrane domain:

amino acids 98-116, 152-172

N-myristoylation site.

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

Glycosaminoglycan attachment site.

amino acids 218-222

FIGURE 5

GGGGCCGCGGTCTAGGGCGGCTACGTGTGTTGCCATAGCGACCATTTGCATTAACGGTTG
 GTAGCTTCTATCCTGGGGCTGAGCGACTGCAGCTCTTCCCTACTCCCTCTCGGCT
 CCTTGTGGCCCAAAGGCCTAACCGGGTCCGGCGGTCTGGCCTAGGGATCTTCCCCGTTGCC
 CCTTGGGGCGGG**ATG**GCTGCGGAAGAAGAACGAGGGTAGTGGAGTGGAGAGCATCG
 CGGGGTTCTCGAGGCCAGACTGGTCCATCCCCATCTGGACTTGTTGGAACAGAAATGT
 GAAGTTAACTGCAAAGGAGGGCATGTGATAACTCCAGGAAGCCCAGAGCCGGTATTGGT
 GGCCTGTGTTCCCTGTTTTGATGATGAAGAAGAAAGCAAATTGACCTATAACAGAGATT
 ATCAGGAATAACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAATT
 AATGAAGATCAATTCAAGAACGATGCACTTCTCCTCTGCAAAGACCCATACATCACAGGC
 CATTGCAACCTGTGTTGGCAGCAGAAGATTACTATCTTAAAGCAATGATGGTCCAGA
 AAAACATTGAAATGCAGCTGCAAGCCATTGAATAATTCAAGAGAGAAATGGTGTATTACCT
 GACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAATCCT
 GAGGGAAAGTTCTTAGAAAATCAAAAGAGGAATATGACCAGGAAGAAGAAAGGAAGAGGAAA
 AACAGTTATCAGAGGCTAAAACAGAACAGCCCACAGTCATTCCAGTGAAGCTGCAATAATG
 AATAATTCCAAGGGATGGTGAACATTGCAACACCCACCCCTCAGAAGTTAAATGCATT
 TGCTAATCAGTCAATAGAACCTTGGAAAGAAAAGTGGAAAGGTCTGAAACTCCTCCCTCC
 CACAAAAAGGCCTGAAGATTCTGGCTTAGAGCATGCGAGCATTGAAGGACCAATAGCAAAC
 TTATCAGTACTTGGAACAGAACACTTCGGCAACGAGAACACTATCTCAAGCAGAACAGAGA
 TAAGTTGATGTCCATGAGAAAGGATATGAGGACTAACAGATAACAAATATGGAGCAGAAAG
 GAAAACCCACTGGGGAGGTAGAGGAAATGACAGAGAACAGAAATGACAGCAGAGGAGAAG
 CAAACATTACTAAAGAGGAGATTGCTTGCAGAGAAACTCAAAGAAGAAGTTATTAATAAG**TA**
ATAATTAAGAACAAATTAAACAAATGGAAGTTCAAATTGTCTAAAAATAATTATTTAGTC
 CTTACACTG

FIGURE 6

MAAEEEDEVEWVVESIAGFLRGPDWSIPILDVFVEQKCEVNCKGGHVITPGSPEPVILVACVP
LVFDDEEESKLTYTEIHQEYKELVEKLLLEGYLKEIGINEDQFQEACTSPLAKTHTSQAILQP
VIAAEDFTIFKAMMVQKNIEMQLQAIRIIQERNGVLPDCLTDGSDVVSDLEHEEMKILREVL
RKSKEEYDQEEERKRKKQLSEAKTEEPTVHSSEAAIMNNSQGDGEHFAHPPSEVKMHFANQS
IEPLGRKVERSETSSLPQKGLKIPGLEHASIEGPLANSLVGTEELRQREHYLKQKRDKLMS
MRKDMRTKQIQNMEQKGKPTGEVEEMTEKPEMTAEEKQTLLKRRLLAEKLKEEVINK

N-glycosylation sites.

amino acids 224-228, 246-250, 285-289

N-myristoylation site.

amino acids 273-279

Amidation site.

amino acids 252-256

Cytosolic fatty-acid binding proteins.

amino acids 78-108

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FIGURE 7

GGGCACAGCACATGTGAAGTTTGATGATGAAGAAGAAAGCAAATTGACCTATAACAGAGAT
TCATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAA
TTAACATGAAGATCAATTCAAGAACCATGCACCTCTCCTCTTGCAGAACCCATAACATCACAG
GCCATTTGCAACCTGTGTTGGCAGCAGAAGATTTACTATCTTAAAGCAATGATGGTCC
AGAAAAACATTGAAATGCAGCTGCAAGCCATTGAATAATTCAAGAGAGAAATGGTGTATTA
CCTGACTGCTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAAT
CCTGAGGGAAGTTCTTAGAAATCAAAAGAGGAATATGACCAGGAA

FIGURE 8

GCGTGGTTTGTTCTGCAATAGGCGGCTAGAGGGAGGGCTTTGCCCTACCTACTG
 TAGCTTCTCCACGTATGGACCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTG
 TCTCAGCTCTAGGATGTGCCTTCCACTAGAAGCTCTGAGGGAGGTAATTAAAAAAC
AGTGGAAATGAAAAACAGTGCCTAGTCATCCTGTAATATGCTCCTGTCAACAATGTATAAC
 ATTCCCTGCTAGGTGCCATTGCTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATT
 CTGCCAATGAAGAAAACAAGTATGATTATCTCCAACACTGTGAATGTGTGCTCAGAACTG
 GTGAAGCTAGTTCTGTGTGCTTGTGTATTAAAGAAAGATCATCAAAGTAG
 AAATTGAAATATGCTCCTGGAAGGAATTCTCTGATTCATGAAGTGGCCATTCCGCCT
 TTCTTATTCTGGATAACTTGATTGTCTTATGCTCTGTCTATCTCAACCAGCCATG
 GCTGTTATCTCTCAAATTAGCATTATAACAAACAGCTCTTCTATTAGGATAGTGCCTGAA
 GAGGCCTAAACTGGATCCAGTGGCTCCCTGCCTGACTTATTGCTATTGTGGCCT
 TGACTGCCGGACTAAAACCTTACAGCACAACTGGCAGGACGTGGATTTCATCACGATGCC
 TTTTCAGCCCTTCAATTCTGCCTCTTCAGAAGTGAGTGTGCCCCAGAAAAGACAATTG
 TACAGCAAAGGAATGGACTTTCTGAAGCTAAATGGAACACCACAGCCAGAGTTTCAGTC
 ACATCCGTCTGGCATGGGCATGTTCTTATATAGTCCAGTGTGTTATTCTCAATGGCT
 AATATCTATAATGAAAAGATACTGAAGGAGGGAACCAAGCCTACTGAAAGCATCTTCATACA
 GAACAGCAAACACTCTATTCTTGCAATTCTGTTAATGGGCTGACTCTGGCCTTCAGAGGA
 GTAACCGTGATCAGATTAGAAACTGTGGATTTTATGCCACAGTGCATTTCAGTAGCC
 CTTATTTGTAACTGCATTCCAGGGCCTTCAGTGGCTTCATTCTGAAGTCCCTGGATAA
 CATGTTCCATGTCTGATGGCCCAGGTTACCACTGTCAATTACAAACAGTGTCTGCCT
 TCTTGACTTCAGGCCCTCCCTGGAATTTCAGTGGCAAGCCCCATCAGTCCTCTCTATA
 TTTATTTATAATGCCAGCAAGCCTCAAGTCCGAATACGCACCTAGGCAAGAAAGGATCCG
 AGATCTAAGTGGCAATCTTGGGAGCGTCCAGTGGGATGGAGAAAGACTAGAAAGACTTA
 CCAAACCCAAGAGTGATGAGTCAGATGAAGATACTTCT**AA**CTGGTACCCACATAGTTGCA
 GCTCTCTGAACCTTATTTCACATTTCAGTGTGTTAATATTATCTTCACTTGATA
 AACCAGAAATGTTCTAAATCCTAATATTCTTGATATCTAGCTACTCCCTAAATGGTT
 CCATCCAAGGCTAGAGTACCCAAAGGCTAAGAAATTCTAAAGAACTGATAACAGGAGTAACA
 ATATGAAGAATTCAATTATCTCAGTACTTGATAAAATCAGAAAGTTATATGTGCAGATTAT
 TTCTTGCCCTCAAGCTCCAAAAACTTGTAAATATCATGTTAGCTATAGCTTGATAT
 ACACATAGAGATCAATTGCCAAATATTACAATCATGTAGTTCTAGTTACATGCCAAAGT
 CTTCCCTTTAACATTATAAAAGCTAGGTTGTCTCTGAATTGGAGGCCCTAGAGATAGT
 CATTGCAAGTAAGAGCAACGGGACCCCTCTAAACAGTTGGTTGAAGGACCTAAATAC
 CTGGCCATACCATAGATTGGGATGATGTAGTCTGTGCTAAATATTGCTGAAGAAGCAGT
 TTCTCAGACACAACATCTCAGAATTAAATTAGAAATTCACTGGAAATTGGATTGTT
 AATAATCTTTGATGTTAAACATTGGTCCCTAGTCACCATAGTTACCACTTGATTTA
 AGTCATTAAACAAGGCCACGGTGGGGCTTTCTCCTCAGTTGAGGGAGAAAATCTTGAT
 GTCATTACTCCTGAATTATTACATTGGAGAATAAGAGGGCATTTATTAGTTACT
 AATTCAAGCTGTGACTATTGTATATCTTCCAAGAGGTGAATGCTGGCTCAGAATCATAC
 CAGATTGTCAGTGAAGCTGATGCCTAGGAACCTTAAAGGGATCCTTCAAAAGGATCACT
 AGCAAAACACATGTTGACTTTAACATTGATGTGAATATTAACTCTAAAGAAGACC
 AGTAATATATAAGTCACTTACAGTGCCTACTCACACTAAAGTGCATGGTATTTCATG
 GTATTTGCATGCAGCCAGTTAACCTCGTAGATAGAGAAGTCAGGTGATAGATGATATTAA
 AAATTAGCAAACAAAAGTGAATTGCTCAGGGCATGCAGCTGGGTGATGATAGAAGAGTGGG
 CTTAACTGGCAGGCCTGTATGTTACAGACTACCATACTGTAAATATGAGCTTATGGTGT
 CATTCTCAGAAACTTATACATTCTGCTCTCCTTCTCCTAAGTTCATGCAGATGAATATA
 AGGTAATATACTATTATATAATTCAATTGATATCCACAATAATGACTGGCAAGAATTG
 GTGGAAATTGTAATTAAAATAATTAAACCT

FIGURE 9

MEKQCCSHPVICSLSTMYTFLLGAIFIALSSSRILLVKYSANEENKYDYLPTTVNCSELVK
LVFCVLVSFCVIKKDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLPAMAV
IFSNFSIITTALLFRIVLKRRLNWIQWASLLTLFLSIVALTAGTKTLQHNLAGRGFHHDAFF
SPSNCLLFRSECPRKDNCATAKEWTFPEAKWNTTARVFSHIRLGGMGHVLIIVQCFISSMANI
YNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTGLQRSNRDQIKNCGFFYGHSAFSVALI
FVTAFQGLSVAFILKFLDNMFHVLMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFI
YNASKPQVPEYAPRQERIRDLSGNLWERSSGDGEELERLTKPKSDESDEDTF

Transmembrane domains:

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293,
298-318, 328-368

N-glycosylation sites.

amino acids 128-132, 204-208, 218-222, 374-378

Glycosaminoglycan attachment site.

amino acids 402-406

N-myristoylation sites.

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

FIGURE 10

CGTGCCTGCGCAATGGGTGTCGGGTCGCTTTCCAATCCGGACGTAATCGTGGTTTG
TTCTGCAATAGCGGCTTAGAGGGAGGGCTTTCGCTATACTACTGTAGCTCTCAC
GTATGGACCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAG
GATGTGCGTTCTTCACTAGAAGCTCTGTGAGGGAGGTAATTAAAAAACAGTGGAAATGGAA
AAACAGTGTGCTGTAGTCATCCTGTAATATGCTCCTGTCAACAATGTATACTACATTCTGCTAGG
TGCCATATTGCTTAAGCTCAAGTCGATCTTACTAGTGAAGTATTGCCAATGAAG
AAAACAAGTATGATTATCTCCAACACTGTGAATGTGTGCTCAGAACTGGTGAAGCTAGTT
TTCTGTGTGCTTGTGTCATTCTGTGTTATAAAGAAAGATCATCAAAGTAGAAATTGAAATA
TGCTTCCTGGAAGGAATTCTCTGATTTCATGAAGTGGCCATTCCCTGCCTTCTTATTC
TGGATAACTGATTGTCTTCTATGTCCTGTCTATCTCAACCAGCCATGGCTGTTATCTC
TCAAATTTAGCATTATAACAACAGCTCTCTATTCAAGGATAGTGCTGAAGAGGCGTCTAAA
CTGGATCCAGTGGGCTTCCCTGACTTATTGTCTATTGTGGCCTTGACTGCCGGGA
CTAAAACCTTA

FIGURE 11

CGGACGCGTGGCGGACGCGTGGCGGACGCGTGGGCCGGCTGGCTAGCGCGCGCGGCC
 GTGGCTAAGGCTGCTACGAAGCGAGCTTGGGAGGAGCAGCGGCCTGCAGGGCAGAGGAGCAT
 CCCGTCTACCAGGTCCAAGCGCGTGGCCCGGGTCATGGCAAAGGAGAAGGGCGAG
 AGCGGCTCCCGGGGGCTGCTACCCACCAAGCATCCTCAAAGCACTGAACGCCGGCCA
 GGTGAAGAAAGAACGAAAAAGAAGAACACAGTTGTCTGTTGCAACAAGCTTGCTATG
 CACTTGGGGAGCCCCCTACAGGTGACGGCTGTGCCCTGGTTCTCCTCAGATCTAC
 CTATTG**GATG**TGGCTCAGGTGGCCCTTCTGCCTCCATCATCCTGTTGTGGCCGAGC
 CTGGGATGCCATCACAGACCCCTGGTGGGCCTCTGCATCAGCAAATCCCCCTGGACCTGCC
 TGGGTCGCCTTATGCCCTGGATCATCTTCTCCACGCCCTGGCGTCATTGCCTACTTCCTC
 ATCTGGTCGTGCCGACTTCCCACACGGCCAGACCTATTGGTACCTGCTTTCTATTGCCT
 CTTTGAAACAATGGTCACGTGTTCCATGTTCCACTCGGCTCTCACCATGTTCATCAGCA
 ACCGAGCAGACTGAGCGGGATTCTGCCACCGCCTATCGGATGACTGTGGAAGTGCTGGCAC
 AGTGCTGGCACGGCGATCCAGGGACAAATCGTGGCCAAGCAGACACGCCCTGTTCCAGG
 ACTTCAATAGCTACAGTAGCTTACAAAGTCCAACCATAACACATGGCACCACAC
 AGGGAAACGAAAAGGCATACCTGTCGGCAGCGGGGTCATTGTCTGTATCTATATAATCTG
 TGCTGTCATCCTGATCCTGGCGTGCAGGAGCAGAGAGAACCCATGAAGCCCAGCAGTCTG
 AGCCAATCGCCTACTTCCGGGCCTACGGCTGGTCATGAGCCACGCCCATACATCAAACCT
 ATTACTGGCTTCCCTTCACCTCCTGGCTTCATGCTGGTGGAGGGAACTTGTCTTGT
 TTGCACCTACACCTGGGCTCCGCAATGAATTCCAGAATCTACTCCTGGCCATCATGCTCT
 CGGCCACTTAACCATTCCCCTGGCAGTGGTCTTGACCCGGTTGGCAAGAACAGCAGCT
 GTATATGTTGGATCTCATCAGCAGTGCCATTCTCATCTGGTGGCCCTCATGGAGAGTAA
 CCTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCCTTAC
 TACCCCTGGTCCATGCTGCCATGTCATTGACGACTTCCATCTGAAGCAGCCCACCTCCAT
 GGAACCGAGCCCATCTTCTCTTCTATGTCTTCCACCAAGTTGCCCTGGAGGTGTC
 ACTGGGATTTCTACCCCTAGTCTGGACTTGCAGGGTACCAAGACCCGTGGCTGCTCGCAGC
 CGGAACGGTCAAGTTACACTGAACATGCTCGTACCATGGCTCCATAGTTCTCATCCTG
 CTGGGCCCTGCTGCTCTTCAAATGTACCCATTGATGAGGAGAGGCGGGCAGAATAAGAA
 GGCCCTGCAGGCACTGAGGGACGAGGCCAGCAGCTGGCTGCTCAGAAACAGACTCCACAG
 AGCTGGCTAGCATCCTC**TAG**GGCCGCCACGTTGCCGAAGCCACCATGCAGAAGGCCACAG
 AAGGGATCAGGACCTGTCGCCGGCTTGCTGAGCAGCTGGACTGCAGGGCTAGGAAGGGAA
 CTGAAGACTCAAGGAGGTGGCCAGGACACTTGCTGCTCACTGTGGGCCGGCTGCTCTG
 TGGCCTCCTGCCTCCCTGCCTGCTGGGCCAGGCCCTGGGCTGCCACTGTGAATA
 TGCCAAGGACTGATGGGCCTAGCCGGAACACTAATGTAGAACCTTTTACAGAGCC
 TAATTAATAACTTAATGACTGTACATAGCAATGTGTGTATGTATGTCTGTGAGCTA
 TTAATGTTATTAATTTCATAAAAGCTGGAAAGC

FIGURE 12

MWLRWALSLPPSSCLWAEPGMPSQT PWWASASANPPGPAWVALCPGSSSPRPWPSLPTSSSG
SCPTSHTARPIGTCFSIASLKQWSRVSMPTRLSPCSSATEQTERDSATAYRMTVEVLGTVL
GTATIQGQIVGQADTPCFQDFNSSTVASQSANHHTGTTSHRETQKAYLLAAGVIVCIYIICAV
ILILGVREQREPYEAQQSEPIAYFRGLRLVMSHGPYIKLITGFLFTSLAFMLVEGNFVLFCT
YTLGFRNEFQNLLLAIMLSATLTIPIWQWFLTRFGKKTAVYVGIISSAVPFLILVALMESNLI
ITYAVAVAAGISVAAAFLLPWMSMLPDVIDDFHLKQPHFHGTEPIFFSFYVFFTAKFASGVSLG
ISTLSLD FAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLGLLLFKMYPIDEERRQNKAL
QALRDEASSSGCSETDSTELASIL

FIGURE 13

GGGAAACGAAAAGGCATACTGCTGGCAGCGGGGTATTGTCTGTATCTATATAATCTGT
GCTGTCATCCTGATCCTGGCGTGCAGGAGCAGAGAGAACCTATGAAGCCAGCAGTCTGA
GCCAATCGCCTACTTCCGGGCCTACGGCTGGCATGAGCCACGGCCCACATCAAACCTTA
TTACTGGCTTCCTCTTCACCTCCTGGCTTCATGCTGGTGGAGGGAACTTGTCTGTT
TGCACCTACACCTGGGCTTCCGCAATGAATTCCAGAATCTACTCCTGGCCATCATGCTCTC
GGCCACTTTAACCATCCCCTGGCAGTGGTCTTGACCCGGTTGGCAAGAAGACAGCTG
TATATGTTGGATCTCATCAGCAGTGCCATTCTCATCTGGTGGCCCTCATGGAGAGTAAC
CTCATCATTACATATCGGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTACT
ACCCTGGTCCATGCTGCCTGATGTCATTGACGACTTCATCTGAAGCAGCCCCACTTCCATG
GAACCGAGCCCAT

FIGURE 14

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTACAAAAGGTGCAGGT
ATGAGCAGGTCTGAAGACTAACATTGTGAAGTTGTAACAGAAAACCTGTTAGAA**ATGT**
GGTGGTTTCAGCAAGGCCTCAGTTCCCTCAGCCCTGTAATTGGACATCTGCTGCT
TTCATATTCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTACCTTATAT
CAGTGACACTGGTACAGTAGCTCCAGAAAATGCTTATTGGGGCAATGCTAAATATTGCGG
CAGTTTATGCATTGCTACCATTATGTTGCTTATAAGCAAGTTCATGCTCTGAGTCCTGAA
GAGAACGTTATCATCAAATTAAACAAGGCTGGCCTGTACTTGGAAACTTGAGTTGTTAGG
ACTTTCTATTGGCAAACCTCCAGAAAACAACCCTTTGCTGCACATGTAAGTGGAGCTG
TGCTTACCTTGGTATGGGCTCATTATATATGTTGTTCAGACCACCTTCCTACCAAATG
CAGCCCCAAATCCATGGCAAACAAGTCTTGGATCAGACTGTTGGTTATCTGGTGTGG
AGTAAGTGCACTTAGCATGCTGACTTGCTCATCAGTTGCACAGTGGCAATTGGGACTG
ATTAGAACAGAAACTCCATTGGAACCCCGAGGACAAAGGTTATGTGCTTCACATGATCACT
ACTGCAGCAGAATGGTCTATGTCATTTCTTCTTGGTTTCTGACTTACATTGTGA
TTTCAGAAAATTCTTACGGTGGAAAGCCAATTACATGGATTAACCCTATGACACTG
CACCTTGCCTATTAACAATGAACGAACACGGCTACTTCCAGAGATATT**TGA**TGAAAGGAT
AAAATATTCTGTAATGATTGATTCTCAGGGATTGGGAAAGGTTCACAGAAGTTGCTTA
TTCTTCTCTGAAATTTCACCCTTAATCAAGGCTGACAGTAACACTGATGAATGCTGATA
ATCAGGAAACATGAAAGAAGCCATTGATAGATTATTCTAAAGGATATCATCAAGAAGACTA
TTAAAAACACCTATGCCTATACTTTTATCTCAGAAAATAAGTCAAAAGACTATG

FIGURE 15

MWWFQQGLSFLPSALVIWTSAAFIFSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNI
AAVLCIATIYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSG
AVLTFGMGSLYMFVQTILSYQMOPKIHGKQFWIRLLLVIWCGVSALSMLTCSSVLHSGNFG
TDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFLTYIRDQKISLRVEANLHGLTLYD
TAPCPINNERTRLLSRDI

FIGURE 16

CGGACGCTTGGGCNGGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGTGCCTGATGCCGAGT
TCCGTCTCTCGGGCTTTCTGGTCCCAGGCAAAGCGGAGCGGAGATCCTCAAACGGCCTA
GTGCTTCGGCTTCCGGAGAAAATCAGCGGCTAATTAAATTCCCTGGTTGTTGAAGCAGT
TACCAAGAACATCTCAACCCCTTCCCACAAAGCTAATTGAGTACACGTTCTGTTGAGTACA
CGTTCCCTGTTGATTACAAAAGGTGCAGGTATGAGCAGGTCTGAAGACTAACATTGTGAA
GTTGTAAAACAGAAAACCTGTTAGAAATGTGGTGGTTCAGCAAGGCCTCAGTTCCCTCCT
TCAGCCCTTGTAAATTGGACATCTGCTGCTTCATATTTCATACATTACTGCAGTAACACT
CCACCATATAGACCCGGCTTACCTATATCAGTGACACTGGTACAGTANC

FIGURE 17

CCCACGCGTCCGCCGCGCTCGTCCCAGTGCAAGTGAGCTCTCGGCTGCCCGCGGG
 CCGGGGTGCAGGCCGACATGCGCCCGCTTCTCGGCCTCCTCTGGTCTCGCCGGCTGCAC
 CTTCGCCTTGTACTTGCTGTCGACCGAAGTGGCTCCGACCTGGCAGAGCTGGCTCCACCGAGG
 AGGCTGGAGGCAGGTCGCTGTGGTCCGACCTGGCAGAGCTGCAGGGAGCTCTCTGAG
 GTCCTTCGAGAGTACCGGAAGGAGCACCGGCCTACGTGTTCTGCTCTGCAGGCCTA
 CCTCTACAAACAGGGCTTGCCATCCCCGGCTCCAGCTTCTGAATGTTTAGCTGGTGCCT
 TGTTGGCCATGGCTGGGCTTCTGCTGTGTTGACCTCGTGGGTGCCACATGC
 TGCTACCTGCTCCAGTATTTGGAACAGTTGGGTGTCCTACTTCCTGATAAAAGT
 GGCCCTGCTGCAGAGAAAGGTGGAGGAGAACAGAAACAGCTGTTTTCTTATTGTTT
 TGAGACTTTCCCCATGACACCAAACGGTTCTGAACCTCTGGCCCCAATTCTGAACATT
 CCCATCGCAGTTCTCTCAGTTATCGGTTGATCCCATAATTCTGTGT
 GCAGACAGGGTCCATCCTGTCAACCCTAACCTCTGGATGCTTTCTCCTGGACACTG
 TCTTTAAGCTGTTGCCATTGCATGGTGGCATTAATTCTGGAACCCCTCATAAAAAATT
 AGTCAGAAACATCTGCAATTGAATGAAACAAGTACTGCTAATCATACACAGTAGAAAAGA
 CACATGATCTGGATTTCTGTTGCCACATCCCTGGACTCAGTGCTTATTGTGAAATGGA
 TGTGGTCCTCTAAAGCCCTCATTGTTTGATTGCCTCTATAGGTGATGTGGACACTGTG
 CATCAATGTGCAGTGTCTTCAGAAAGGACACTCTGCTCTGAAGGTGATTACATCAGGT
 TTTCAAACCAGCCCTGGTGTAGCAGACACTGCAACAGATGCCTCTAGAAAATGCTTTGT
 GGCGGGCGCGGTGGCTACGCCTGTAATCCAGCAGCTTGGAGGCCGAGGCCGGTATTG
 ACAAGGTCAAGGAGTTCAAGACCAGCCTGGCCAAGATGGTGAATCCTGCTCTAATAAAAT
 ACAAAAATTAGCCAGGCAGGTGGCAGAGGTTGCAAGCCAAGATCACACCACTGCACT
 AGGAGAATTGCTTGAACCAAGGTGGCAGAGGTTGCAAGCCAAGATCACACCACTGCACT
 CCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

FIGURE 18

MRPLLGLLVFAGCTFALYLLSTRLPRGRRLGSTEAGGRSLWFPSDLAELRELSEVLREYR
KEHQAYVFLFCGAYLYKQGFAIPGSSFLNVLAGALFGPWLGLLLCCVLTSGATCCYLSS
IFGKQLVVSYFPDKVALLQRKVEENRNSLFFFLFLRLFPMTPNWFLNLSAPILNIPIVQFF
FSVLIGLIPYNFICVQTGSILSTLTSLDALFSWDTVFKLLAIAMVALIPGTLIKKFSQKHLQ
LNETSTANHIHSRKDT

Important features:

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 101-123, 189-211

N-glycosylation sites.

amino acids 172-176, 250-254

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 240-244, 261-265

N-myristoylation site.

amino acids 13-19, 104-110, 115-121, 204-210

Amidation site.

amino acids 27-31

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 4-15

Protein splicing proteins.

amino acids 25-31

Sugar transport proteins.

amino acids 162-172

FIGURE 19

CCGAGGCAGGGAGGAGCCCCGAGGGGGCGCGAGCCCCGATGAATCATTGTAGTCAATCATTTC
CCAGTTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTCCGAACGCCAGCTCAGAA
TAGGAAAATAACTTGGGATTTATATTGGAAGAC**ATG**GATCTTGCTGCCAACGAGATCAGCA
TTTATGACAAACTTCAGAGACTGTTGATTGGTGAGACAGACCGGCCATCAGTGTGGCATG
TCAGAGAAGGCAATTGAAAAATTATCAGACAGCTGCTGGAAAAGAATGAACCTCAGAGACC
CCCCCGCAGTATCCTCTCCTTATAGTTGTATAAGGTTCTCGAACCTGGGATTAATCT
TGCTCACTGCCTACTTGTGATTCAACCTTCAGCCCATTAGCACCTGAGCCAGTGCTTCT
GGAGCTCACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCCTGCCATTGCCAA
GAAGTACATGTCAGAAAATAAGGGAGTTCCCTGCATGGGGGTGATGAAGACAGACCCCTTC
CAGACTTGACCCCTGGTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCCATTCTGCC
AACTGCACTGGCTGTGCCAGAAACACCTGAAGGTGATGCTCCTGGAAGACGCCAAGGAA
ATTGAGAGGCTCCATCCACTGGTGATCAAGACGGAAAGCCCTGTTGGAGGAAGAGATTG
AGCATTGGCCAGTACCCCTGAGGCGACAGAAGGCTCTGAAGGGTTTCGCCAAG
TGGTGGCGCTGCTTCCTGAGCGGTGGTCCATTCCATTCCATGGAGGAGACCTCTGAA
CAGATCACAAATGTTACGTGAGCTTCTGTTCACTCACCTGCCATTCCAAAAGATG
CCTCTTAAACAAGTGCTCCTTCTCACCCAGAACCTGTTGGGGAGTAAGATGCATAAG
ATGCCTGACCTATTTATCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTCCA
GTGCCGAAGACATTGTCAGTCTGTGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTG
ACACCACCCACTGGAAGGTCTACGTATAGCCAGAGGGTCCAGCCTTGGTCATCTGCGAT
GGAACCGCTTCTCAGAACTG**TAG**GAAATAGAACTGTGCACAGGAACAGCTCCAGAGCCGA
AAACCAGGTTGAAAGGGAAAAATAAAAACAAAAACGATGAAACTGCAAAAA

FIGURE 20

MDLAANEISIYDKLSETVDLVRQTGHQCGMSEKAIEKFIRQLLEKNEPQRPPPQYPLLIVVY
KVLATLGLILLTAYFVIQPFSPLAEPVLSGAHTWRSЛИHHIRLMSLPIAKKYMSENKGVPL
HGGDEDRPFDPFWWTNDCEQNESEPI PANCTGCAQKHLKVMILLEAPRKFERLHPLVIKT
GKPLLEEEIQHFLCQYPEATEGFSEGFFAKWWRCFPERWFPPYPWRRPLNRSQMLRELFPV
FTHLPFPKDASLNKCSFLHPEPVVGSKMHKMPDLFIIGSGEAMLQLI PPFQCRRHCQSVAMP
IEPGDIGYVDTTHWKVYVIARGVQPLVICDGTAFSEL

FIGURE 21

CCACGGTGTCCGTCTTCGCCGGCGCAGCTGTCCCCGAGGCAGGAGGCCGAGGGCG
CGAGCCCCGATGAATCATTGTAGTCAATCATTTCAGTTCTCAGCCGTTCAGTTGTGATC
AAGGGACACGTGGTTCCGAACTGCCAGCTCAGAATAGGAAAATAACTTGGGATTATATT
GGAAGACATGGATCTTGCTGCCAACGAGATCAGCATTATGACAAACTTCAGAGACTGTTG
ATTTGGTGAGACAGACCGGCCATCAGTGTGGCATGTCAGAGAAGGCAATTGAAAAATTATC
AGACAGCTGCTGGAAAAGAACCTCAGAGACCCCCCGCAGTATCCTCTCCTTATAGT
TGTGTATAAGGTTCTCGAACCTTGGGATTAATCTTGCTCACTGCCTACTTGTGATTCAAC
CTTCAGCCCATTAGCACCTGAGCCAGTGCTTGTGGAGCTCAC

FIGURE 22

CCCACGCGTCCGCCAACGCGTCGGCTGAACACCTCTTGGAGTCAGCCACTGATGAGG
 CAGGGTCCCACTTGCAGCTGCAGCAGCTGCAGCAGCTGCTCCTGGCTGGTG
 CCACTGGTGCACGCTGCTAGACCGTGCCTATGAGCCGTGGGCTGCAGTGGGACTGCC
 CTCCCTGCCACCCACCAATGGCAGCCCCACCTTCTTGAAGACTTCCAGGCTTTGTGCCA
 CACCCGAATGGCGCCACTTCATCGACAAACAGGTACAGCCAACCATGTCAGTCCAGTTGCAAATG
 GACACGTATGCTAAGAGCCACGACCTTATGTCAGGTTCTGGAATGCCCTGCTATGACATGCT
 TATGAGCAGTGGCGAGCGGGCCAGTGGAGCGCCAGACTCGTCGGGCCTTCAGGAGC
 TGGTGTGGAACCTCGCAGAGGCGGGCGCCTGGAGGGCTACGCTACACGGCAGTGTG
 AAGCAGCAGGCAACGCAGCACTTCCATGGGCCCTGCTGCACTGGGGCGCTGTGGCGCCAGCT
 CGCCAGCCCATGTGGGCCCTGGCGCTGAGGGACACTCCCATCCCCGCTGAAACTGTCCA
 GCGCCGAGACATATTACGCATGCGCTGAAGCTGGTCCCCAACCATCACTCGACCCCTCAC
 CTGGAAGCCAGCGCTCTCGAGACAATCTGGGTGAGGTTCCCCGTACACACCACCGAGGAGGC
 CTCACTGCCTCTGGCAGTGACCAAAGAGGCCAAAGTGAGCACCCCACCCGAGTTGCTGCAGG
 AGGACCAGCTCGCGAGGAGCAGCTGGCTGAGCTGGAGACCCGATGGAGGCAGCAGAACTG
 GATGAGCAGCGTGAGAAGCTGGTGTGTCGGCCAGTGCCAGCTGGTAGCAGGTAGTGGCGT
 GGTCCCAGGGCTGCTGGAGGTACACACAGAAATGTATACTTCTACGATGGCAGCAGTGCAGC
 GCGTGGAAACCGAGGGAGGCCATCGGCTATGATTCCGGCCACTGGCCAGCTGCGTGAG
 GTCCACCTCGCGGGCTTCAACCTCGGCCCTGAGCAGTCTTATCGATCAGGC
 CAACACTTCTCAACTTCCATGCAAGGTGGCAGCACCCAGCTCATCTCTAGCCAGA
 CTCCGAGACCCCAGCTGGCCCCATCCCACCCATACCCAGGTACGGAACCCAGGTGTACTCG
 TGGCTCTGCGCTACGGCCCCCTCTCAAGGCTACCTAAGCAGCCGCTCCCCCAGGAGAT
 GCTCGTGCCTCAGGCCTACCCAGAAATGGGTACAGCGTGAGATATCCAACCTCGAGTACT
 TGATGCAACTCAACACCATTGCGGGCGGACCTACAAATGACCTGTCTCAGTACCCGTGTT
 CCCTGGGTCTGAGGACTACGTGTCCCCAACCCCTGGACCTCAGCAACCCAGCCGTCTCCG
 GGACCTGTCTAAGCCCATCGGTGTGGTAACCCCAAGCATGCCAGCTCGTGAGGGAGAACT
 ATGAAAGCTTGAGGACCCAGCAGGGACATTGACAAGTTCCACTATGGCACCCACTACTCC
 AATGCAAGCAGGGCGTGTGACTACCTCATCCCGCTGGAGGCCCTCAGCTCCCTGACGTCCA
 GCTGCAAAGTGGCGCTTGTACTGCTCCGACGGCAGTCCACTCGGTGGCGAGCCTGG
 AGGCACCGCTGGAGAGCCCTGCCGATGTGAAGGAGCTCATCCCGGAATTCTACTTCT
 GACTTCTGGAGAACCAAGAACGGTTTGACCTGGCTGTCTCCAGCTGACCAACGAGAAGGT
 AGGCATGTGGTGTACCCCGTGGCCAGCTCTCTGAGGACTTCATCCAGCAGCACCGCC
 AGGCTCTGGAGTCGGAGTATGTGTCTGCACACCTACAGAGTGGATGACCTCATTTGGC
 TACAAGCAGCGGGGGCAGCCGCCAGGAGGCCCTCAATGTCTCTATTACTGCACCTATGA
 GGGGGCTGTAGACCTGGACCATGTGACAGATGAGCGGAAACGGAAGGCTCTGGAGGGCATT
 TCAGCAACTTGGCAGACTCCCTGTCAGCTGCTGAAGGAGCCACATCCAACACTCGGCTCTCA
 GCTGAGGAAGCAGCCCATCGCTTGACGCCCTGGACACTAACCTACCTAGCATCTCCAGCA
 CCTGGAGCAACTCAAGGCATTCTCGCAGAGGTGACTGTGAGTGCCAGTGGCTGTGGCA
 CCCACAGCTGGTGCCTATGACCGCAACATAAGCAACTACTTCAGCTCAGCAAAGACCCC
 ACCATGGGCAGCCACAAGACGCAGCGACTGCTGAGTGGCCCTGGGTGCGAGGAGTGGTGT
 GAGTGGACAAGCACTGGCAGTGGCCCCGGATGGAAAGCTGCTATTCAAGCGGTGGCAGTGGG
 ATGGCAGCCTGCGGGTGACTGCACTACCCCGTGGCAAGCTGTTGAGCCAGCTCAGTGCCAC
 CTTGATGTAGTAACCTGCCCTGCACTGGACACCTGTGGCATCTACCTCATCTCAGGCTCCCG
 GGACACCACGTGCATGGTGTGGCGGCTCTGCATCAGGGTGGCTGTCACTAGGCTGGC
 CAAAGCTGTGCAGGTCTGTATGGGATGGGCTGCAGTGAGCTGTGTGGCCATCAGCACT
 GAACTTGACATGGCTGTCTGGATCTGAGGATGGAACCTGTGATCATACACACTGTACGCC
 CGGACAGTTGTAGCGGCAACTACGGCTCTGGGTCACATTCCCTGGACCTATTTCACC
 TGGCATTGGGGTCCGAAGGGCAGATTGTGGTACAGAGCTCAGCGTGGGAACGTCCTGGGGC
 CAGGTCACTACTCCTGACCTGTATTCACTGCAATGGGAAGTGTGCGGGCTTCAGTGC
 GGCAGAGCAGCCTACAGCCCTGACGGTGACAGAGGACTTGTGTTGCTGGCACCGCC
 GCGCCCTGCACATCCTCAAACACACTGCTCCCGGCCGCGCTCCCTGCCATGAAG
 GTGGCCATCCGCGCGTGGCGCTGACCAAGGAGCGCAGCCACGTGCTGGTGGGCTGGAGGA
 TGGCAAGCTCATCGTGGTGGTGCAGGGCGAGCCCTCTGAGGTGCGCAGCAGCCAGTTCGC
 GGAAGCTGTGGCGGTCTCGCGCGCATCTCCAGGTGTCCTCGGGAGAGACGGAATACAAC
 CCTACTGAGGCGCGCT**TGA**ACCTGGCCAGTCCGGCTGCTCGGGCCCCGCCGGCAGGCCTG
 GCCCGGGAGGCCCCGCCAGAAGTCGGCGGGAACACCCCGGGGTGGGCAGCCCAGGGGTGA
 GCGGGGGCCACCCCTGCCAGCTCAGGGATTGGCGGGGATGTTACCCCTCAGGGATTGGCG
 GCGGGAAGTCCCCCTCGCGGCTGAGGGGCCGCCCCCTGAGGGGCCAGCACTGGCGTCT

FIGURE 23

MSQFEMDTYAKSHDLMMSGFWNACYDMLMSSGQRQWERAQSRRAFQELVLEPAQRARLEG
RYTAVLKQQATQHSMALLHWGALWRQLASPCGAWLRTPIPRWKLSSAETYSRMRLKLVPN
HHFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDELAELET
PMEAAELDEQREKLVLSAECQLVTVVAVVPGLEVTTQNVFYDGSTERVETEEGIGYDFRRP
LAQLREVHLRRFNLRRSALELFFIDQANYFLNFPCKVGTPVSSPSQTPRPQPGPIPHTQV
RNQVYSWLLRLRPPSQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQLNTIAGRKYNDL
SQYPVFPWVLQDYVSPTLDLSNPNAVFRDL SKPIGVVNPKHAQLVREKYESFEDPAGTIDKFH
YGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDCSDRQFH VAAAWQARLES PADVKELIP
EFFYFPDFLENQNGFDLGCLQLTNEKVGDVVLPPWASSPEDFIQQHRQALESEYVSAHLHEW
IDLIFGYKQRGPAAEEALNVFYYCTYEGAVDLDHVTDERERKALEGIISNFGQTPCQLLKEP
HPTRLSAEEAAHRLARLDTNSPSI FQHLDELKAFFAEVTVSASGLLGTHSWLPYDRNISNYF
SFSKDPTMGSHKTQRLLSGPWVPGSGVSGQALAVAPDGKLLFSGGHWDGSLRVTAI PRGKLL
SQLSCHLDVVTCLALDTCGIYLISGSRDTTCMVWRLHQGGLSVGLAPKPVQVLYGHGA AVS
CVAISTELDMAVSGSEDGTVI IHTVRRGQFVAALRPLGATFPGP IFHLALGSEGQIVVQSSA
WERPGAQVTYSLHLYSVNGKL RASLPLAEQPTALTVDFTVLLGTAQC ALHILQLNTLLPAA
PPLPMKVAIRSVAVTKERSHVLVGL EDGKLIVVVAGQPSEVRSSQFARKLWRSSRRISQVSS
GETEYNPTEAR

N-glycosylation site.

amino acids 677-681

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 985-989

Tyrosine kinase phosphorylation site.

amino acids 56-65, 367-376, 543-551

N-myristoylation site.

amino acids 61-67, 436-442, 604-610, 610-616, 664-670, 691-697,
706-712, 711-717, 769-775, 785-791, 802-808, 820-826, 834-840,
873-879, 912-918, 954-960

FIGURE 24

CGGACGCGTGGCGGACGCGTGGGGCTGTGAGAAAGTCCAATAAATACATCATGCAACCC
 CACGGCCCACCTTGTGAACTCCTCGTGCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCAT
 CCAAAGGCCTAATCCAACGTTCTGTCTTCATCTGCAAATCTATGGGTCCTGGGGCTCTTC
 TGGACCCTTAACGGGTACTGGCCCTGGGCCAATGCGTCCTCGCTGGAGGCCCTTGCCCTCCTT
 CTACTGGGCCTTCCACAAGCCCCAGGACATCCCTACCTCCCTTAATCTCTGCCTTCATCC
 GCACACTCCGTTACCACACTGGTCATTGGCATTGGAGGCCCTCATCCTGACCCTGTGCAG
 ATAGCCCCGGGTATCTGGAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCTGTAGC
 CCGCTGCATCATGTGCTGTTCAAGTGCTGCCCTGGTGTCTGGAAAAATTATCAAGTTCC
 TAAACCGCAATGCATACATCATGATGCCATCTACGGGAAGAATTCTGTGTCTAGCCAAA
 AATGCGTTCATGCTACTCATGCGAACATTGTCAGGGTGGTCGTGGACAAAGTCACAGA
 CCTGCTGCTGTTCTGGGAAGCTGCTGGTGGTCGGAGGGCGTGGGGCTCTGTCCTTCTTT
 TTTTCTCCGGTCGCATCCGGGCTGGTAAAGACTTAAGAGCCCCCACCTCAACTATTAC
 TGGCTGCCCATCATGACCTCCATCCTGGGGCTATGTCATGCCAGCGGCTTCTCAGCGT
 TTTCGGCATGTGTGGACACGCTTCCCTGCTTCTGGAGACCTGGAGCGGAACAACG
 GCTCCCTGGACC GCCCTACTACATGTCCAAGAGCCTCTAAAGATTCTGGCAAGAAC
 GAGGCGCCCGGACAACAAGAAGAGGAAGAAGTGACAGCTCCGGCCCTGATCCAGGACTGC
 ACCCCACCCCCACCGTCCAGCCATCCAACCTCACTTCGCCTTACAGGTCTCCATTGTGGT
 AAAAAAAGGTTTAGGCCAGGCGCCGTGGCTCACGCCTGTAATCCAACACTTGAGAGGCTG
 AGGCGGCGGATCACCTGAGTCAGGAGTTGAGACCAGCCTGGCCAACATGGTAAACCTCC
 GTCTCTATTAAAAATACAAAAATTAGCCAGGAGTGGTGGCATGCACCTGTCATCCAGCTAC
 TCGGGAGGCTGAGGCAGGAGAACGCTTGAACCCGGAGGCAGAGGTTGCAGTGAGCCGAGA
 TCGGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAACAAACAA
 AAAGATTAAAGATATTGTAACTC

FIGURE 25

RTRGRTRGGCEKVPINTSCNPTAHVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVLGLF
WTLNWVLALGQCVLAGAFASFYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQ
IARVILEYIDHKLRGVQNPKVARCIMCCFKCCLWCLEKFIFLNRNAYIMIAIYGKNFCVSAK
NAFMLLMRNIVRVVVLDKVTDLLLFFGKLLVVGGVGVLSSFFFSGRIPGLGKDFKSPHLNYY
WLPIMTSILGAYVIASGFFSVFGMCVDTLFLCFLEDLERNNNGSLDRPYYMSKSLLKILGKKN
EAPPDNKKRKK

FIGURE 26

GAGTCTTGACCGCCGCCGGCTTGGTACCTCAGCGCAGGCCAGGCGTCGGCGCCGT
 GGCT**ATG**TTCGTGTCCGATTCCGCAAAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGTCC
 TTCTCTCGTGGCCTCGGACGTGGATGCTGTGCGTGCAAGATCCTCAGGCCTTGTTC
 CAGTGTGACCACGTGCAATATACTGGTCCAGTTCTGGTGGCAAGAACTTGAAACTGC
 ATTTCTTGAGCATAAAGAACAGTTTCAATTCTCATAAACTGTGGAGCTAATGTAG
 ACCTATTGGATATTCTAACCTGATGAAGACACTATATTCTTGTGTGACTCCCATAGG
 CCAGTCAATGTCGTCAATGTATAAACGATAACCCAGATCAAATTACTCATAAACAAGATGA
 TGACCTTGAAGTTCCCGCCTATGAAGACATCTCAGGGATGAAGAGGAGGATGAAGAGCATT
 CAGGAAATGACAGTGTGGTCAGAGCCTCTGAGAACGCGCACACGGTTAGAAGAGGAGATA
 GTGGAGCAAACCATGCGGAGGGAGGCAGCGGAGAGTGGAGGCCGGAGAACAGACATCCT
 CTTTGACTACGAGCAGTATGAATATCATGGACATCGTCAGCCATGGTATGTTGAGCTGG
 CTTGGATGCTGTCCAAGGACCTGAATGACATGCTGTGGTGGCCATCGTGGACTAACAGAC
 CAGTGGGTGCAAGACAAGACTCAAATGAAATACGTGACTGATGTTGGTGTCCCTGCAGCG
 CCACGTTCCCGCCACAACCACCGAACGAGGATGAGGAGAACACACTCTCCGTGGACTGCA
 CACGGATCTCCTTGAGTATGACCTCCGCTGGTGTCTACCAGCACTGGTCCCTCCATGAC
 AGCCTGTGCAACACCAGCTACCGCAGCCAGGTTCAAGCTGTGGTGTGCATGGACAGAA
 GCGGCTCCAGGAGTTCTGCAGACATGGTCTTCCCTGAAGCAGGTGAAGCAGAACAGTTCC
 AGGCCATGGACATCTCCTGAAGGAGATTGCGGGAAATGATTGAAGAGTCTGCAAATAAA
 TTTGGGATGAAGGACATGCGGTGCAAGACTTCAGCATTCAAGCATTGGGTCAAGCACAAGTT
 TCTGGCCAGCGACGTGGTCTTGCACCATGTCTTGATGGAGAGCCCCGAGAACGGATGGCT
 CAGGGACAGATCACTCATCCAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTG
 TACCATGGCCTGGAACTCGCCAAGAACGAGCAGCTGCGAGCCACCCAGCAGACCAATTGCCAGCTGC
 CTTTGACCAACCTCGTCATCTCCAGGGCCTTCCGTACTGCTCTCATGGAGGGCAC
 TCCAGATGTCTGTTCTAGGCCGGATCCCTAACGCTGCTCAGCAAACACCTGCTCA
 AGTCCTTGTGTGTCGACAAAGAACCGGCCTGCAAACGTGCTGCCCTGGTATGGCTGCC
 CCCCTGAGCATGGAGCATGGCACAGTGACCGTGGTGGCATCCCCCAGAGACCGACAGCTC
 GGACAGGAAGAACCTTTGGGAGGGCGTTGAGAAGGCAGCGAAAGCACCAGCTCCCGGA
 TGCTGCACAACCATTGACCTCTCAGTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTT
 CTGGACGCACCTATTCCCTCTGTCCT**TAG**GAATTGATTCTCCAGAAATGACCTCTTATT
 TATGTAACTGGCTTCATTAGATTGTAAGTTATGGACATGATTGAGATGTAGAACGCCATT
 TTTTATTAAATAAAATGCTTATTAGGAAA

FIGURE 27

MFVSDFRKEFYEVVQSQRVLLFVASDVLCACKILQALFQCDHVQYTLVPVSGWQELETAFL
LEHKEQFHYFILINCGANVDLLDILQPDEDTIFFVCDSHRPVNVVNVYNDTQIKLLIKQDDD
LEVPAYEDIFRDEEDEEHSGNDSDGSEPSEKRTRLEEEIVEQTMRRQRREWEARRDILF
DYEQYEYHGTSSAMVMFELAWMLS KDLNDMLWWAIVGLTDQWVQDKITQMKYVTDVGVLQRH
VSRHNHRNEDEENTLSVDCTRISFEYDLRLVLYQHWSLHDSDLNTSYTAARFKLWSVHGQKR
LQEFLADMGLPLKQVKQKFQAMDISLKENLREMIEESANKFGMKDMRVQTFSIHFGFKHKFL
ASDVVFATMSLMESPEKDGS GTDHFIQALDSLSRSNLDKLYHGLELAKKQLRATQQTIASCL
CTNLVISQGPFLYCSLMEGTPDVMLFSRPASLSLLSKHLLKS FVCSTKNRRCKLLPLVMAAP
LSMEHGTVTVVGIPPETDSSDRKNFFGRAFEKAAESTSSRMLHNHF DLSVIELKAEDRSKFL
DALISLLS

FIGURE 28

GTACCTCAGCGCGAGCGCCAGGCAGCGTCCGGCCGCCGTGGCTATGNTCGTGTCCGATTCCGCA
AAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCCTCTCTCGTGGCCTCGGANGTGGAT
GCTCTGTGTGCGTGCAAGATCCTCAGGCCTTGTCCAGTGTGACCANGTGAATATANGCT
GGTCCAGTTCTGGGTGGCAAGAACTTGAAACTGCATTCTTGAGCATAAAGAACAGTTTC
ATTATTTATTCTCATAAACTGTGGAGCTAATGTAGACCTATTGGATATTCTAACCTGAT
GAAGACACTATATTCTTGTGTGACACCCATAGGCCAGTCAATGTTGTCAATGTATAACAA
CGATAACCC

FIGURE 29

CAGGAACCTCTTGGGTCTGGATTGGGACCCCTTCCAGTACCATTTCTAGTGAAC
 CACGAAGGGACGATACCAGAAAACACCCCAACCCAAAGGAAATAGACTACAGCCCCAATTG
 GCTGACTTTGGCTATAGAAAAAAGAAAGGAACGAAAAGAGACAGTTTTGGAAAGCTAA
 GTCTTCCCTTATCGAGTCAGAAACCCCCCTTCTTGAGCTATTAACAGCTTTAACAAATT
 GAGTAAAGTACGCTCCGGTCAACC**ATG**GTGACAGCCGCCCTGGTCCCCTGGGCAGCGCTC
 CTGCTCTTCTCCTGATGTGAGATCCGTATGGTGGAGCTCACCTTGACAGAGCTGTGGC
 CAGCGGCTGCCAACGGTGTGACTCTGAGGACCCCTGGATCCTGCCATGTATCCTCAG
 CCTCTTCCCTCCGGCCGCCAACGCCCTGCCATGAGATCAGACCCTACATTAAATACACCATC
 CTGAAGGGTACAAAGGGGACCCAGGCCCCAATGGGCCTGCCAGGGTACATGGGCAGGGAGGG
 TCCCCAAGGGGAGCCTGGCCCTCAGGGCAGCAAGGGTACAAGGGGAGATGGGCAGCCCCG
 GCGCCCCGTGCCAGAAGCGCTTCTTCGCCTCTCAGTGGGCCAGAACGCCCTGCACAGC
 GGCGAGGACTTCCAGACGCTGCTCTCGAAAGGGTCTTGTGAACCTTGATGGGTGCTTGA
 CATGGCGACCGGCCAGTTGCTGCTCCCTGCGTGGCATCTACCTCTTCAGCCTCAATGTGC
 ACAGCTGGAATTACAAGGAGACGTACGTGCACATTATGCATAACCAGAAAGAGGCTGTGTCATC
 CTGTACCGCGAGCCCAGCGAGCGCAGCATCATGCAGAGCCAGAGTGTGATGCTGGACCTGGC
 CTACGGGACCGCGTCTGGTGCCTCAAGGCCAGCGCAGAACGCCATCTACAGCA
 ACGACTTCGACACCTACATCACCTCAGGCCACCTCATCAAGGCCAGGGACGACT**TGA**GGG
 CCTCTGGGCCACCCCTCCCGCTGGAGAGCTCAGGTGCTGGTCCCGTCCCTGCAGGGCTCAG
 TTTGCACTGCTGTGAAGCAGGAAGGCCAGGGAGGTCCCCGGGGACTGGCATTCTGGGGAGA
 CCCTGCTCTCATCTGGCTGCCATCATCCCTCCAGCCTATTCTGCTCTCTTCTCT
 TGGACCTATTAAAGAAGCTGCTAACCTAAATATTCTAGAACATTCCAGCCTCGTAGCCC
 AGCACTTCTCAAACATTGAAATGCATGCGAATCACCCGGGTTCGTGTAAATGCAGATTCT
 GACTCAGCAGGTCTGAGTGGTCCAGGATTCTGTGTTCTCATATGTTCTGGGTGATGCTG
 ATGGGGTCAGTCTATGAACCACACTGGAGCAACCAGGTTCTAGGACTTTCTCAATATTCTAG
 TACTTCTGAACATTCTGGAATCCTCCCCACATTCTAGAATTCTCCAACATTTTTTCT
 TGAGACAGAGTCTGCTCTGTTGCCAGGCTAGAGTGCAGTGGTCAACTCAGTCAGTCACTGC
 AACCTCTGCCCTCCGGTTCAAGCGATTCTCTGCCCTAGCCTCCCTAGTGGCTGGGATTAC
 AGGCCTGCTGCTACCATGCCCTGGTAATTCTGTATTAGTAGAGATGGGGTTTACCCATA
 TTGGCCAGGCTGGTCTTGAACTCCTGACTTCAGGTGACCCACCCGCCCTGGCCTCTCAAAAT
 GCTGGGATTACAGGTGTGAGCCACCGTGCCTGCCATTCCAACATTCTAAATTCTCTCAT
 CCCTCCAGGGCTCCCGTGTATGTTCTTACCCCTCCCTCTTGCTCAGGCC
 TGACCAACTGCAGCCACCGTTATTATTCAATTAAACACTGAGCACTCACTCTGTGCT
 GGGTCCCGGAAGGGTGAGGGGGTCAGACACAGGCCCTGCCCTGCCCTAGTGAATGGCCA
 GTCCAGCCCAGGCCGGAGAGATGTGATAGGTTAAAGCAGACCCAGAGCTCATGGGG
 GCCTGTGTTCTGGGTGTTCAAGGTGCTGCTGGCCTCCATTACCCACTGCTCCCCAAGGCTGG
 TGGGACGGGGTCCCGGTGGCAGGGCAGGTATCTCTTCCCTGCCATCCACCTGCCAG
 TGCTCATCGTTACAGCAAACCCAGGGGGCTTGGCCAGGTCAAGGGTTCTGTGAGGAGAGG
 ACCCAGGAGTGTGGGGCATTTGGGGGTGAAGTGGCCCCGAAGAATGAAACCCACACCCA
 TAGCTCTCCCCACAGCTGATACGGCATCCTGCCAGAACACTGCCCTCCTCACTGGGATCCC
 CTTCTGCCCTCCCTCCAGGGCTCTGCCAGGGCCTTGCTCAGTCCTTCAACCAAAGTCATCT
 GAACTCCGTTCCCCAGGGCTCCAGCTGCCCTCAGACACTGATGTCAGTGTCCCCAGGTGCT
 CTCTGCCCTCATGCCCTCTCACCGGCCAGTGCCTCAGAGCCCTCCGGCCTGGTGTGCTGCCCTTAC
 CTAAGGCCGGTGGCAGCTCCTCGTCTCAGAGCCCTCCGGCCTGGTGTGCTGCCCTTAC
 AAACACCTGCAGGAGAAGGGCACGGAAGGCCAGGCCTTAGAGCCCTCAGCAGGTCTGGGG
 AGCTAGAGCAAGGGAGGGACCTCAGGCCTCCGTTCTTCAGGGTGGGGTGGCCTGGT
 GTTCCCCTAGCCTCCAAACCCAGGTGGCCTGCCCTCTCCCCAGAGGGAGGGCAGGCCCTCCGC
 CCATTGGGTGCTCATGCAGACTCTGGGGCTGAGGTGCCCTGGGGGTGATCTCTGGTGTGCTCAC
 AGCCGAGGGAGCCGTGGCTCCATGCCAGATGACGGAACAGGGTCTGACCAAGTGCAGGA
 AGACCTGTGCTATAAACACCCCTGCTGATCCTGCCCTGCCCTGACCCGCCACGCCCTGCC
 GTCCAGCATGATTAAAGAATGCTGTCCTCTGGAAAAAAAAAAAAAA

FIGURE 30

MVTAALGPVWAALLFLLMCEIRMVELTDRAVASGCQRCCDSEDPLDPAHVSSASSSGRPH
ALPEIRPYINITILKGDKGDPGPMGLPGYMGREGPQGEPGPQGSKGDKGEMGSPGAPCQKRF
FAFSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMATGQFAAPLRGIYFFSLNVHSWNYKET
YVHIMHNQKEAVILYAQPSERSIMQSQSVMMLAYGDRVWVRLFKRQRENAIYSNDFDTYIT
FSGHLIKAEDD

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 72-75

C1q domain proteins.

amino acids 144-178, 78-111 and 84-117

FIGURE 31

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCTCGGGCCCGACCCGCCAGGAAAGACTG
 AGGCCGCGGCCTGCCCCGCCGGCTCCCTGCGCCGCCCTCCCAGGACAGAAG**ATGTG**
 CTCCAGGGTCCCTTGCTGCTGCCGCTGCTCTGCTACTGGCCCTGGGGCTGGGTGCAGG
 GCTGCCCATCCGGCTGCCAGTGCAGCCAGCACAGACAGTCTCTGCAC TGCCGCCAGGG
 ACCACGGTCCCCGAGACGTGCCACCCGACACGGTGGGCTGTACGTCTTGAGAACGGCAT
 CACCATGCTCGACGCAGGCAGCTTGCCGGCTGCCGGGCTGCAGCTCTGGACCTGTAC
 AGAACCAAGATGCCAGCCTGCCAGCGGGTCTTCCAGCCACTGCCAACCTCAGAACCTG
 GACCTGACGGCCAACAGGCTGCATGAAATACCAATGAGACCTCCGTGGCCTGCCGCCT
 CGAGCGCCTCACCTGGCAAGAACCGCATCCGCCACATCCAGCCTGGTGCCTCGACACGC
 TCGACCGCCTCCTGGAGCTCAAGCTGCAGGACAACGAGCTGCAGGGCACTGCCCGCTGC
 CTGCCCGCCTGCTGCTGGACCTCAGCCACAACAGCCTCCAGGAGCCGGCAT
 CCTGGACACTGCCAACCTGAGCTGGAGGCCTGCCGGGCTGCAGCCTGGAGCTGGAGC
 AGGGCTCTTCAGCCGCTTGCACCTCCACGACCTGGATGTGTCCGACAACCAGCTGGAG
 CGAGTGCCACCTGTGATCCGAGGCCTCCGGGCTGACGCCCTGCCGGCTGGCGAACAC
 CCGCATTGCCAGCTGCCGGCGAGGACCTGCCGGCCTGGCTGCCCTGCCAGGAGCTGGATG
 TGAGCAACCTAACGCTGCAGGCCCTGCCCTGGCAGCCTCTGCCCGCTTCCCCCGCTGC
 CTGCTGGCAGCTGCCGCAACCCCTCAACTGCGTGTGCCCGCTGAGCTGGTTGCCCGCT
 GGTGCCGAGAGCCACGTACACTGCCAGCCCTGAGGAGACGCCCTGCCACTTCCC
 AGAACGCTGCCGGCTGCTCTGGAGCTGACTACGCCACTTGGCTGCCAGCACCACC
 ACCACAGCCACAGTGCCAACCACGAGGCCCTGGTGCGGGAGCCCACAGCCTGTCTTAG
 CTTGGCTCCTACCTGGCTAGCCCCACAGGCCGGCACTGAGGCCCGAGGCCCTCCA
 CTGCCCAACCGACTGTAGGGCCTGTCCTCCAGGCCAGGACTGCCACCGTCCACCTGC
 CTC AATGGGGCACATGCCACCTGGGACACGGCACCACCTGGCGTCTGTGCCCGAAGGCTT
 CACGGGCTGTACTGTGAGAGCCAGATGGGGCAGGGACACGCCAGCCCTACACCAGTCA
 CGCCGAGGCCACCACGGTCCCTGACCCCTGGGATCGAGCCGGTGA
 GAGCCCCACCTCCCTGCC
 GTGGGGCTGCAGCGTACCTCCAGGGAGCTCCGTGAGCTCAGGAGCCTCCGTCTCAC
 TCGCAACCTATCGGGCCCTGATAAGCGGCTGGTACGCTGCGACTGCCCTGCTCGCTG
 AGTACACGGTCAACCGACTGCCAACGCCACTTACTCCGTCTGTGTCATGCC
 CTTGGGGCTGTACTGTGAGAGCCAGATGGGGCAGGGACACGCCAGCCCTACACCAGTCA
 CTCCAACCACGCCAGTCACCCAGGCCGAGGGCAACCTGCCCTCCTCATTGCC
 CCCTGGCCGCCGGTGCCTCTGGCCGCCGCTGGCTGCCGGGGCAGCCTACTGTG
 CGGGGCCATGGCAGCAGCGCTCAGGACAAAGGGCAGGTGGGGCAGGGCTGGGCC
 GGAACACTGGAGGGAGTGAAGGTCCCCCTGGAGGCCAGGCCGAAGGCAACAGAGGG
 CGGTGGAG
 AGGCCCTGCCAGCGGGCTGAGTGTGAGGTGCCACTCATGGGCTCCAGGGCTGGC
 C
 CAGTCACCCCTCCACGCAAAGCCCTACATC**TAA**AGGCCAGAGAGAGACAGGG
 CAGCTGGGCC
 GGCTCTCAGCCAGTGAAGATGCCAGGCCCTCCCTGCTGCCACACCACGTAAGT
 TCTCAGTCC
 CAACCTCGGGGATGTGTCAGACAGGGCTGTGTGACCA
 CAGCTGGGCCCTGTTCCCTCTGG
 CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGCC
 TAACGTC
 CGAGTGCCTATGAGGACAGTGTCCGCCCTGCCCTCGCAACGTGCA
 GTCAGTCCCTGGGAC
 CGGCC
 GGCCCTGCCATGTGCTGGTAACGCA
 GCCTGGGCTCTCC
 CACTGCCAGGG
 CGGA
 CCCTGGGGGCCAGTGAAGGAAGCTCCGGAAAGAGCAGAGGGAGAGCGGG
 TAGGCC
 GTG
 TGACTCTAGTCTGGCCCAAGGAAGGAAC
 AAAAGAAACTGGAAAGGAAGATGCTT
 TA
 GGAACATGTTTGCTTTTAA
 AATATATATTTATAAGAGATCCT
 CCCATTATTCTG
 GGAAGATGTTTCAA
 ACTCAGAGACAAGGACTTGGTTTGTAAGAC
 AACAGTGA
 ATGATATG
 AAGGC
 CTTTGT
 AAGAAAAA
 AAAAAAGATGA
 AGTGT
 GAAA

FIGURE 32

MCSRVPLLLPLLLALGPGVQGCPSCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVFEN
GITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETFRGLR
RLERLYLGKNRIRHIQPGAFDTLDRILLEKLQDNELRALPPLRLPRLLLLDLSHNSLLALEP
GILDGTANVEALRLAGLGLQQQLDEGLFSRLRNLDVSDNQLERVPPVIRGLRGLTRLRLAG
NTRIAQLRPEDLAGLAALQELDVSNLSQLAPGDLSGLFPRRLAAARNPFNCVCPLSWFG
PWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTATVPTTRPVVREPTALS
SSLAPTWLSPTAPATEAPSPPSTAPPTVGVPQPQDCPPSTCLNGGTCHLGTRHHACLCPE
GFTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGLQRYLQGSSVQLRSLRL
TYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHTPPA
VHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRAMAAAQDKGQVGPAG
PLELEGVKVPLEPGPKATEGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI

FIGURE 33

GAATCATCCACGCACCTGCAGCTCTGCTGAGAGAGTGAAGCCGGGGGGTTTGGAGCTCAT
 CTTCATCATTATGAGGAAATAAGTGGAAAATCCTGGAAATACA**ATG**AGACTCATCAG
 AAACATTACATATTTGTAGTATTGTTAGCAGCAGAGGGTATGCTCCAGAGCTGCCAG
 AAGAAAGGAACTGATGACCAACTGCTCCAACATGTCTAAGAAAGGTTCCCAGACTTG
 ACCCCAGGCCAACGACACTGGATTATCCTATAACCTCCTTTCAACTCCAGAGTCAGA
 TTTTCATCTGTCTCCAAACTGAGAGTTTGATTCTATGCCATAACAGAAFTCAACAGCTGG
 ATCTCAAACCTTGAATTCAACAAGGAGTTAAGATATTAGATTGTCTAATAACAGACTG
 AAGAGTGTAACTTGGTATTACTGGCAGGTCTCAGGTATTAGATTGTCTTAAATGACTT
 TGACACCATGCCATCTGTGAGGAAGCTGCCAACATGTCACACCTGGAAATCCTAGGTTGA
 GTGGGGCAAAATCACAAATCAGATTCCAGAAAATTGCTCATCTGCATCTAAATACTGTC
 TTCTTAGGATTAGAACTCTCCTCATTATGAAGAAGGTAGCCTGCCATCTAAACACAAAC
 AAAACTGCACATTGTTTACCAATGGACACAAATTCTGGGTTCTTGCCTGATGGAATCA
 AGACTTCAAAATATTAGAAATAGACAAATATAGATGGAAAAGCCAATTGTAAGTTATGAA
 ATGCAACGAAATCTTAGTTAGAAATGCTAAGACATCGGTTCTATTGCTTAATAAGTTGA
 TTTACTCTGGGACGACCTTTCCTTATCTTACAATTGTTGGCATACTCAGTGGAAACACT
 TTCAGATCCGAAATGTGACTTTGGTGGTAAGGCTTATCTGACCACAATTCTGACTAC
 TCAAATACTGTAATGAGAACTATAAAATTGGAGCATGTACATTTCAGAGTGTTTACATTCA
 ACAGGATAAAATCTATTGCTTGGACCAAAATGGACATAGAAAACCTGACAATATCAAATG
 CACAAATGCCACACATGCTTCCGAAATTATCCTACGAAATTCCAATATTAAATTGGCC
 ATAATATCTAACAGCAGATTGTTAAAAGAACTATCCAACCTGCCACTTGAAAACCTCT
 CATTGAAATGGCAATAAAACTGGAGACACTTCTTAGTAAGTTGCTTGCCTAACACAC
 CCTTGGAACACTTGGATCTGAGTCAAAATCTATTACACATAAAATGATGAAATTGCTCA
 TGGCCAGAAACTGTGGTCAATATGAATCTGTCATACAATAATTGTCGATTCTGCTTCAG
 GTGCTTGGCCAAAGTATTCAAATACTGACCTAAATAACCAATCCAAACTGTACCTA
 AAGAGACTATTCATCTGATGGCCTACGAGAACTAAATTGCTATTCTAACTGAT
 CTCCCTGGATGCAGTCATTCTAGTAGACTTCTGAACTTGAACATTGAAACTTCATTCT
 CAGCCCCATCTGGTACCTGGTCAAGCTGCCAGGAAGTAAAACCTAAATGCGGGAAAGAA
 ATCCATTCCGGTGTACCTGTGAATTAAAAAAATTCTACAGCTTGAACATATTGAGGTC
 ATGATGGGGATGGTCACTTCAACACCTGTGAATACCTTTAACCTAAGGGAAACTAG
 GTTAAAAGACGTTCATCTCACGAATTATCTGCAACACAGCTCTGTTGATTGTCACCATTG
 TGGTTATTATGCTAGTTGGGGTTGGCTGTCCTGCTGTCCTTGTGATCTGCC
 TGGTATCTCAGGATGCTAGGTCAATGCACACAAACATGGCACAGGGTTAGGAAACACCA
 AGAACAACTCAAGAGAAATGTCGATTCCACGCATTATTACAGTGAACATGATTCTC
 TGTGGGTGAAGAATGAATTGATCCCCAATCTAGAGAAGGAAGTGGTCTATCTGATTG
 CTTTATGAAAGCTACTTGAACCTGGCAGGAAAGCTTGTCAAGTGAACATGTTCTATTGA
 GAAAAGCTATAAGTCCATTTGTTGCTCCACACTTGTCAAGTGAACATGTTCTATTGA
 ATGAATTCTACTTTGCCACACATCTTCCATGAAATTCTGATCATATAATTCTTATC
 TTACTGGAACCCATTCCATTCTATTGCTATTCCACAGGTATCATAAACTGAAAGCTCTCCT
 GGAAAAAAAGCATACTTGAATGGCCAAGGATAGGCGTAAATGTTGGCTTTCTGGCAA
 ACCTTCGAGCTGCTATTATGTAATGTTAGGCCACAGAGAAATGATGAACTGCAGACA
 TTCACAGAGTTAAATGAAGAGTCTCGAGGTTCTACAATCTCTGATGAGAACAGATTGTCT
A**TAA**AAATCCCACAGTCCTGGGAAGTTGGGACCATACACTGTGGGATGTACATTGATA
 CAACCTTATGATGGCAATTGACAATATTAAATAAAAATGGTTATTCCCTTCATA
 TCAGTTCTAGAAGGATTCTAAGAATGTATCCTATAGAAACACCTCACAAGTTATAAGG
 GCTTATGGAAAAAGGTGTTCATCCCAGGATTGTTATAATCATGAAAATGTGGCCAGGTG
 AGTGGCTCACTCTGTAATCCCAGCAGTGGGAGGCAAGGGTGGGTGACCCACGAGGTCAA
 GAGATGGAGACCATCCTGGCCAACATGGTGAACCCCTGCTCTACTAAAAAATACAAAAATT
 GCTGGGGCTGATGGTGCACGCCGTGAGTCCAGCTACTTGGGAGGCTGAGGCAGGAGAAATCG
 CTTGAACCCGGGAGGTGGCAGTTGCAAGTGTGAGATCGAGGCCACTCCAGCCTGGT
 GACAGAGCGAGACTCCATCTAAAAAAAGAAAAAAAGAAAAAAATGGAAAACATCC
 TCATGGCCACAAAATAAGGTCTAATTCAATAATTATAGTACATTAATGTAATATAATT
 CATGCCACTAAAAGAATAAGGTAGCTGTATATTCTGGTATGGAAAAACATATTAAAT
 GTTATAAAACTATTAGGTTGGTGCAGAAACTAATTGTTGGTTGGCATTGAAATGGCATTGAA
 ATAAAAGTGTAAAGAAATCTACCAAGATGTAGTAACAGTGGTTGGGCTGGGAGGTTGGA
 TTACAGGGAGCATTTGATTCTATGTTGTATTCTATAATGTTGAATTGTTAGAATGA
 ATCTGTATTCTTTATAAGTAGAAAAAAATAAGATAGTTTACAGCCT

FIGURE 34

MRLIRNIYIFCSIVMTAEGDAPELPEERELMTNCNSMSLRKVPADLTATTLDLSYNLLFQ
LQSSDFHSVSKRLVLILCHNRIQQQLDLKTFEFNKELRYLDLSNNRLKSVTWYLLAGLRYLDL
SFNDFDTMPICEEAGNMSHLEILGLSGAKIQKSDFQKIAHLHLNTVFLGFRTLPHYEEGSLP
ILNTTKLHIVLPMDTNFWVILLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLL
LNKVDLLWDDLFLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFR
VFYIQQDKIYLLLTKMDIENLTISNAQMPHMLFPNYPTKFQYLNFANNILTDELFKRTIQLP
HLKTLILNGNKLETLSVSCFANNTPLEHLDLSQNLLQHKNDENCSWPETVVNMNLSSYNKLS
DSVFRCLPKSIQILDLNNNQIQTVPKETIHLMALRELNIAFNFLTDLPGCSHFSRSLSVLNIE
MNFILSPSLDFVQSCQEVKTLNAGRNPFRCTCELKNFIQLETYSEVMMVGWSDSYTCEYPLN
LRGTRLKDVLHHELSCNTALLLIVTIVVIMLVLGLAVAFCCLHFDLPWYLRLMLGQCTQTWHRV
RKTTQEQLKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSISENI
VSFIEKSYKSIFVLSNFVQNEWCHYEFYFAHHNLFHENDHIIILILLEPIPFYCIPTRYHK
LKALLEKKAYLEWPKDRRKCGFWANLRAAINVNVLATREMYELQFTTELNEESRGSTISLM
RTDCL

FIGURE 35

GGGGGCTTCTTGGGCTTGGCTGCTTGGAACACCTGCCTCCAAGGACCGGCCCTGGAGGGTCGCCGGAAAGG
 GAGGAAGAAGGAAGGGCGGGGCCGGCCCCCTGCGCCCGCCCCCGCCTCTGCGGCCCTGTCCGCCGGC
 CCAGCCCAGCCCAGCCCCCGGGCGGTACACCGCGAGCCAGCCAGGCCCTCCCGGCCAAGCGCGCGCT
 CTGCTGTGCCCTGCGCCCTTGCCCCCGCAGCTTCTGCGCCCGCAGCCGCCGGCGCCCGGTGACCGTGA
 CCCTGCCCTGGCGGGGCCGGACAGGC**ATG**TCCCGCCCGGGACCGTACCCAGCCTGGCCCTGGTGTCTC
 CTGGCAGTGAACCTGGCCGGGTCGGAGCCCAGGGCGCAGCCCTCGAGGACCTGATTATTACGGGAGGAGAT
 CTGGAGCCGGAGCCCTACTACCGCGCCCGAGCCCGAGCTCGAGACCTCTCCGCCGTGCCTGCCGGC
 CCGGGGAGGAGTGGGAGCGGCCGAGGCCAGGGGCCAACAGGGCACCAAGCCAAGAAAGCTCCC
 AAGAGGGAGAAGTCGGCTCCGGAGCCCTCCACCAGTAAACACAGCAACAAAAAGTTATGAGAACCAAGAG
 CTCTGAGAAGGCTGCCAACGATCATCACAGTGTCCGTGAGGCTTGTGAGGAGAGTTGCCACCTC
 TTGGTCTGAAACCTAAAAATCACAGACTCCAGCTCCATGCCCTCACGGTCAAGCGCTATGCCCTGGGGCA
 CATCGAGGGAGACTAACATCCAGCGGGCATTATGAAAATGATTTTATGACGGAGCGTGTGCGCCGGAG
 AAATGACCTCCAGCAGTGGATTGAAGTGGATGCTGGCCCTGACAGATTCACTGGTGTGTCATCACTCAAGGGAG
 GGAACCTCCCTGGCTGAGTGAATGGGACATCCTATAAGGTGAGGAGATCCCTGTTCTCAATGAGCT
 ACTGTTAAGAATGGGACATGATATTGAGGGAAACAGTGGAGAAGGAGATGCCCTGTTGATAATGGGAGCATTGAGCT
 ACCCGTCCCCATGGGGCCGCTACATCCGCTAAACCTCAGTCTGGTTGATAATGGGAGCATTGAGCT
 GAATGGAGATCCTGGCTGCCACTGCCAGATCCTAATAATTATTACCCGCCAACAGAGATGACCACCACT
 GATGACCTGGATTAAAGCACACAATTATAAGGAAATGCCAGTTGATGAAAGTTGATGAAATGTC
 CAATATCACCAGAATTACACATTGGAAAAGCCACCAGGGCTGAAGCTGATGCTGAGGAGATCTCAGATC
 ACCCTGGGGAGCATGAAGTCGGTGAGCCGAGTCCACTACATGCCGGGGGCCACGGCAATGAGGTGCTGGG
 CGGGAGCTGCTGCTGCTGGTGAGTTCTGTGTCAGGAGTACTGGCCCGGAATGCCGCATGTCACCT
 GGTGGAGGAGACGCCGATTACGTCTCCCTCCCTCAACCCCGATGGCTACGAGAACGGCTACGAAGGGGCT
 CGGAGCTGGAGGCTGGCCCTGGGACGCTGGACCCACGATGGAATTGACATCAACAACAACTTCTGATT
 AACACGCTGCTCTGGAGGCAGAGGATCGACAGAAATGCCCCAGGAAAGTCCCAACTACTATGCAATCCC
 TGAGTGGTTCTGTCGAAAATGCCACGGTGGCTGCCAGACAGAGCTCATAGCCTGGATGGAAAAAAATCC
 CTTTGTGCTGGCGCAACCTGCAGGGCGGAGCTGGTGGCTGCCGTATCCCTACGACTGGTGGCTCCCC
 TGGAGACGCAGGAACACACCCCCACCCCGATGACAGCACGTTCCGTGGCTGCGCTACTCCTATGCCCTCCAC
 ACACCGCCCTCATGACAGACGCCGGAGGGTGTGCCACAGGGAGACTCCAGAAGGAGGGCACTGTCA
 ATGGGGCCTCTGGCACACCGTGCCTGGAAGTCTGAACGATTCTACCTTACACAAACTGCTCGAAGTG
 TCCATCTACGTGGCTGTGATAAAATACCCACATGAGAGCCAGCTGCCGAGGAGTGGGAGAATAACGGGAATC
 TCTGATCGTGTTCATGGAGCAGGTTCATCGTCGGATTAAAGGCTGGTGGAGGATTACATGGAAAAGGAATC
 CAAACGCCATTATCTCGTAGAAGGCATTACCATGACATCCGACAGCAACGATGGGATTACTGGCGCCTC
 CTGAACCTGGAGAGTATGTTGTCACAGCAAAGGCCAAGGTTCACTGCATCCACCAAGAAACTGATGGTT
 CTATGACATGGGGCCACAAGGTTGACTTACACTAACCAACATGCCAGGATCCGAGAGATCATGG
 AGAAGTTGGGAAGCAGCCGTCAGCCTGCCAGGCCAGGGCTGAAGCTGCCGGGGCGGAAGAGACAGCGT
 GGG**TG**AACCTCTGGCCCTTGAGACTCGTCTGGACCCATGCAAATTAAACCAACCTGGTAGTACGCTCATAG
 TGGACTCACTCACTGTTGTTCTCTGTAATTCAAGAAGTGCCTGGAAGAGAGGGTGCATTGTGAGGCAGGTCC
 CAAAAGGAAAGGCTGGAGGCTGAGGCTGTTTCTTGTCCATTATCAAATAACTGGACAGAGCA
 GCAGAGAAAAGCTGATGGAGTGGAGAAGTCAAGCAAGCCAACCTGGGAATCAGAGAGAGAAGGAGAAGGAGGG
 GAGCCTGTCGCTCAGAGCCTCTGGCTGCATAGAAAAGGATTCTGGTGTCTCCCTGTTGCGTGGCAGCAAGG
 GTTCCACGTGCATTGCAATTGACAGCTAAATTGACGCTTCCCGAGCTGGCTGTCCCAAATGTTACCA
 TTTGAGATGCTCCAGGCGCTCTAACAGAACATCCACCCCTCTGCCCTGGGACATTGCAAGCTGCTACAAATA
 ATTCTGTTCTTGTGACAATAGCGTATTGCCAAGTGCACATCAGTGAGGCCCTTGAATCTGTTAGTCTCCT
 TTTCAACAAAGGAGTGTGTTGAGAAAAGGAGAGAGGGCTGAGATCATTGAGGATTGTTGGCAGCAAGCA
 TGGAGCTCTTGACAAATTCTGGGCTCATAAACACCCCCAAAGTCCCTGCTGATCCAGTAGCCCTGGAGGTT
 CCCCAGGTAGGGAGAGCCAGGGTGCCTGCAAGGGCAGAAAATTAGCCTGGATCTCTTAC
 CTGCTAGGACTGGAAAGAGCCAGAAGTGGGCTGAGGCCCTCTGCTTGAGGTATTGCCCTGTGTG
 GAATTGAGTGCTCATGGGTTGCCCTATATCAGCCTGGAGTTATTGATATGAGAATGCCAGATCTTCCA
 GATTAGGCTAAATGTAATGAAACCTTCTAGGATTATCTGTTGAGCATTGAGTTGGGAGAAGATTATTGAATTAT
 CTTGCAAGAAAAAGTATGTCCTACTTTGTTAATGTTGCTGCCCTATTGACCTGGGAAAGAATGAAATT
 AATAAAGCAAATGGTAAGACCCCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 36

MSRPGTATPALALVLLAVTLAGVGAQGALEDPDYYGQEWSREPYYARPEPELETFSPP
AGPGEWERPQEPRPKRATPKKKAPKREKSAPEPPPGKHSNKKVMRTKSSEKAANDHS
VRVAREDVRESCPPLGLETLKITDFQLHASTVKRYGLGAHRGRNLNIQAGINENDFYDGAWCA
GRNDLQQWIEVDARRLTRFTGVITQGRNSLWLSDWVTSYKVMVSNDSHTWTVKNGSGDMIF
EGNSEKEIPVNLNPVPMVARYIRINPQSFDNGSICMRMEILGCPLPDNNYYHRRNEMTT
TDDLDFKHHNYKEMRQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHPGEHEVGEPEF
HYIAGAHGNEVLGRELLLLVQFVCQEYLARNARIHLVEETRIHVLP SLNPDGYEKAYEGG
SELGGWSLGRWTHDGIDINNNFPDLNTLLWEAEDRQNVPRKVPNHYIAIPEWFLSENATVAA
ETRAVIAWMEKIPFVLGGNLQGGELVVAYPYDLVRSPWKTQEHTPTPDDHVFRWLAYSYAST
HRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFSYLHTNCFELSIYVGCDKYPHES
QLPEEWENNRESLIVFMEQVHRGIKGLVRDSSHGKGIPNAIIISVEGINDIRTANDGDYWRL
NPGEYVVTAKAEGFTASTKNCMVGYDMGATRCDFTLSKTNMARIREIMEKFGKQPVSLPARR
LKLRGRKRRORG

FIGURE 37

CTAAGAGGACAAC **ATG**AGGCCGGCCTCTCATTTCTCTAGCCCTCTGTTCTCCCTGGCCAAGCTGCAGGG
 ATTTGGGGATGTGGGACCTCCAATTCCCAGCCCCGGCTTCAGCTCTTCCAGGTGTTGACTCCAGCTCCAGC
 TTCAAGCTCCAGCTCAGGTGGGCTCCAGCTCCAGCCAGCTAGGCAGCGGAGGTTCTGTGTCAGCTT
 TTCAATTACCGGCTCCGTGGATGACCGTGGGACCTGCCAGTGTCTGTTCCCTGCCAGACACCACCTTC
 CCGTGGACAGAGTGGAACGCTTGAATTACAGCTCATGTTCTCAGAAGTTGAGAAAGAACCTTCTAAA
 GTGAGGGAAATATGTCCAATTAAATTAGTGTGATGAAAAGAACCTGTTAACCTAAGTGTCCGAATTGACATCAT
 GGAGAAGGATAACCAATTCTTACACTGAACCTGGACTTCGAGCTGATCAAGGTAGAAGTGAAGGAGATGGAAAAAC
 TGGTCATACAGCTGAAGGAGAGTTGGTGGAGCTCAGAAATTGTTGACCAAGCTGGAGGTGGAGATAAGAAAT
 ATGACTCTTGGTAGAGAACGCTTGAGACACTAGACAAAAAACAAATGTCCTTGCCATTGCCAGAAATCGTGGC
 TCTGAAGACCAAGCTGAAAGAGTGTGAGGGCTCTAAAGATCAAACACCCCTGTCGTCCACCCCTCCCACTC
 CAGGGAGCTGTGGTCAATGGTGGTGGTGAACATCAGCAAACCGCTGTGGTCAACTGGAGAGGGTT
 TCTTATCTATGGTGGCTTGGGATTACTCTCCCAGCATCCTAACAAAGGACTGTATTGGGTGGC
 ATTGAATACAGATGGAGACTGTTGGAGTATTATAGACTGTACACACACACTGGATGATTGCTATTGTATATAA
 ATGCTCGAGAGTTGGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTACAACAAACATGTACGTCAAC
 ATGTACAACACCGGAATTGGCAGACTTAACCTGACCAACACGATTGCTGTGACTCAAACCTCCCTAA
 TGCTGCCTATAATAACCGCTTTCATATGCTAATGTTGCTTGGCAAGATATTGACTTTGCTGTGGATGAGAATG
 GATTGTGGTTATTATTCAGTGAAGGCCAGCTGGTAACATGGTGATTAGTAAACTCAATGACACCACACTT
 CAGGTGCTAAACACTGGTATACCAAGCAGTATAAACCATCTGCTTCTAACGCCCTCATGGTATGTGGGTTCT
 GTATGCCACCCGTACTATGAACACCAAGAAGAGATTTTACTATTATGACACAAACACAGGGAAAGAGG
 GCAAACATAGACATTGTAATGCATAAGATGCAGGAAAAGTGCAGAGCATTAACTATAACCCTTTGACCAGAAA
 CTTTATGCTATAACGATGGTACCTCTGAATTATGATCTTCTGTCTGAGAACGCCAG **TAA**GCTGTTA
 GGAGTTAGGGTAAAGAGAAAATGTTGAAAAAATAGTCTTCTCACTTACTTAGATATCTGCAGGGGTGT
 CTAAAAGTGTGTTCTTGCAGCAATGTTAGGTGCATAGTTCTACCACACTAGAGATCTAGGACATTGTC
 TGATTGGTAGTTCTTGGGAATCATCTGCCTCTCAGGCGCATTGCAATAAGTGTCTAGGGTGGGA
 TTGTCAGAGGTCTAGGGCACTGTGGCTAGTGAAGCCTACTGTGAGGAGGCTTCACTAGAACCTTAAATTA
 GGAATTAAAGGAACCTAAACTCAGTATGGCTCTAGGGATTCTTGTACAGGAAATATTGCCAATGACTAGTC
 CTCATCCATGAGCACCCTAACTCTCCATGCCCTGGAAGAACCTGGGACTTAGTTAGGTAGATTAATATCT
 GGAGCTCCCTGAGGGACCAAATCTCAACTTTTCCCCTCACTAGCACCTGGAATGATGCTTGTATGTGG
 CAGATAAGTAAATTGGCATGCTTATATATTCTACATCTGAAAGTGTGAGTTATGGAGAGAGGCCCTTTT
 ATGCATTAATTGTACATGGCAATAATCCCAGAAGGATCTGTAGATGAGGCACCTGCTTTCTTCTCTC
 ATTGTCCACCTTACTAAAGTCAGTAGAATCTCTACCTCATAACTCCTCCAAAGGCAGCTCAGAAGATTAG
 AACCAAGACTACTAACCAATTCCACCCCCCAGCAACCCCCCTACTGCCTACTTTAAAAAAATTAAATAGTTT
 CTATGAAACTGATCTAAGATTAGAAAATTAAATTCTTAAATTCTCATTATGGACTTTATTCATGACTCTA
 AGACTATAAGAAAATCTGATGGCAGTGACAAAGTGTAGCATTATTGTTATCTAATAAGACCTGGAGCATA
 TGTGCAACTTATGAGTGTATCAGTTGTTGCATGTAATTTCGCTTGTGTTAACGCTGGAACCTGTAAGAAAAT
 GAAAATTAAATTCTTCTAGGACGAGCTATAGAAAAGCTATTGAGAGTATCTAGTTAATCAGTGCAGTAGT
 TGGAAACCTTGCTGGTGTATGTGATGTGCTTGTGCTTTGAATGACTTTATCATCTAGTCTTGTCTATT
 TCCCTTGTGTTCAAGTCCTAGTCTATAGGATTGGCAGTTAAATGCTTTACTCCCCCTTAAATAAATGAT
 TAAAATGTGCTTGAaaaaaaaaaaaaaaaaaaaaaaa

FIGURE 38

MRPGLSFLLALLFFLGQAAGDLGDVGPIPSPGFSSFPGVDSFFFSSSRSGSSSRSLGS
GGSVSQLFSNFTGSVDDRGTQCQCSVLPDTTFPVDRVERLEFTAHVLSQKFEKELSKVREYV
QLISVYEKLLNLTVRIDIMEKDTISYTELDFELIKVEVKEMEKLVIQLKESFGGSSEIVDQ
LEVEIRNMTLLVEKLETLDKNNVLAIRREIVALKTKLKECEASKDQNTPVVHPPPTPGSCGH
GGVVNISKPSVVQLNWRGFSYLYGAWGRDYSQHPNKGLYWVAPLNTDGRILLEYYRLYNTLD
DLLLYINARELRITYGQGSGTAVYNNNMYVNMYNTGNIARVNLTNTIAVTQTLPNAAAYNNR
FSYANVAWQDIDFAVDENGLWVIYSTEASTGNMVISKLNDTTLQVLNTWYTKQYKPSASNAF
MVCGVLYATRTMNTRTEEIFYYYDTNTGKEGKLDIVMHKMQEKVQSINYNPFDQKLYVYNDG
YLLNYDLSVLQKPO

FIGURE 39

GCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCTCTAAAGATCAAACACCCCTGTCGTCCAC
CCTCCTCCCACCTCCAGGGAGCTGTGGTCATGGTGGTGTGGTGAACATCAGCAAACCGTCTGT
GGTCAGCTCAACTGGAGAGGGTTTCTTATCTATGGTCTGGGTAGGGATTACTCTC
CCCAGCATCCAAACAAAGGNATGTATTGGGNNGGCCATTGAATACAGATGGGAGACTGTTG
GAGTATTATAGACTGTACAACCCACTGGATGATTGCTATTGTATATAATGCTCGAGAGTT
GC GGATCACCTATGCCAAGGTAGTGGTACAGCAGTTACAACAACATGTACGTCAACA
TGTACAACACCGGGNATATTGCCAGAGTTAACCTGACC

FIGURE 40

TCTCGCAGATAAGTAAATAATCTCGGAAAGGCAGAGAAAAGAGCTGTCTCCATCTGTCTGT
CCGCTGCTTTGTGACGGTGTGGAGATGGGGAGCGCTGGGCTGTGCTCATGGCGAGCT
GGATACCAGTGTGGAAGTGCCCCGTGTTGCTATGCCGATGCTGCTCATAGTGGAAAC
AACTCCACTGTAACTAGATTGATCTATGCACTTTCTTCTGCTGGAGTATGTAGCTTG
TGTAAATGTTGATACCAGGAATGGAAGAACAACTGAATAAGATTCCCTGGATTGGTGGAGAATG
AGAAAGGTGTTGTCCTGTAACATTTGGTGGCTATAAGCTGTATATGTTGCTTGGCTT
GGTTGGCTATGTTCTATCTCTCTTACTAATGATCAAAGTGAAGAGTAGCAGTGA
TCCTAGAGCTGCAGTCACAATGGATTGGTCTTAAATTGCTGCAGCAATTGCAATT
TTATTGGGCATTCTCATCCAGAAGGAACCTTACAAGTGTGGTTATGTAGGCATG
GCAGGGCCTTGTCTCATCCTACACAACAGTCTTACTATTGATTGACATTGACATTG
GAATGAATCGTGGGGTGAAGGGAACTCGAGATGTTGGTATGCAGCCTGT
TATCAGCTCACAGCTGAAATTATCTGCTGCTTTAGTTGCTATCGTCTGTTCTGTAC
TACACTCATCCAGCCAGTGTTCAGAAACAAAGGGCCTCATCAGTGTCAACATGCTCCTGT
CGTGGTGTCTGTAAATGCTATACAGTCAACAAATGTTGACATGGTCAGCTATGACCAAT
TGTTACAGTCTCAGTAATTACAGTCTACACAATGTTGACATGGTCAGCTATGACCAAT
GAACCAAGAAACAAATTGCAACCCAAGTCTACTAACGATAATTGGCTACAATACAAAGCAC
TGTCCAAAGGAAGGGCAGTCAGTCAGTGGTGGCATGCTCAAGGAATTAGGACTAATT
TCTTTTGTGTGTATTATTCCAGCATCCGTACTTCAAACAAATAGTCAGGTTAATAAA
CTGACTCTAACAAAGTGTAAATCATAATTAGAAGATGGGGAGCTAGAAGTGATGGATC
ACTGGAGGATGGGACGATGTTCACCGAGCTGTAGATAATGAAAGGGATGGTGTCACTTACA
GTTATCTCTCTTCACTCATGCTTTCTGGCTCACTTATATCATGATGACCCCTTAC
AACTGGTCCAGGTATGAAACCTCTCGTGAGATGAAAGTCAGTGGACAGCTGTCTGGTGA
AATCTCTCCAGTTGGATTGGCATCGTGTGTTGGACACTCGTGGCACACTTGTTC
TTACAAATCGTATTGAC**TGA**GTGAGACTTCTAGCATGAAAGTCCACTTGTATTG
TTATTGAAACAGTATTCCAACTTTGTAAAGTGTGTATGTTGCTTCCATGTAAAC
TTCTCAGTGTCTGGCATGAATTAGATTACTGCTGTCTATTGTTATTTCTTACAA
GTGCATTGATATGTGAAGTAGAATTGAGAGGAAAGTTTATGAATATGGTGTGAGT
TAGTAAAAGTGGCATTATTGGCTTATCTCTGCTCTATAGTTGAAATGAAGAGTAAA
ACAAATTGTTGACTATTAAATTATATTAGACCTTAAGCTGTTAGCAAGCATTAA
GCAAATGTATGGCTGCCTTGTAAATTGATGTTGCTGGCAGGATACTGCAAAGAAC
ATGGTTATTAAATTATAAACAAAGTCACTTAAATGCCAGTTGTGAAAAATCTTATA
AGGTTTACCCCTGATACGGAATTACACAGGTAGGGAGTGTGTTAGTGGACAATAGTGAGG
TTATGGATGGAGGTGTCGGTACTAAATTGAAATAACAGAGTAATACTTACTTGGGAGAGA
TGGCCTTGCACAAAGTGAACCTGTTGTTAAACTCATGAAAGTATGGGTCAGT
GGAATGTTGAAACTCTGAAGGATTAGACAAGGTTGAAAGGATAATCATGGGTTAGA
AGGAAGTGTGAAAGTCATTGAAAGTTAGTTGGGCCCAGCACGGTAGCTCACCCTT
GGTAATCCCAGCACTTGGGAGCTTAAGTGGTAGATTACTGAGCCCAGGAATTGAGACCA
GCTTGGCACATGGTGAACCTGTTCTATAAAATAATCTGGCTTGGACATATGCTGTGTC
CAGCACTGAGAGGCTAGTGAAGATTGCTGAGCCCAGGCCAAAGGTTGCAAGTGAGCAAGTC
CGTCACTGCACCTAGCTGGCACAGAGTAAGCCAAAAAAATATATATATTGAAATCAAGG
AGGCAAAATTGACAGGGAGGAAGTAACAGTCAAAACCACTAGGCTTAGTAGGTA
ATAAAATCTAGTCCAGTCTCTCATTTAAAAAAATGAAGACACTGAAATAACAGACTTAA
GCTCAGATAGCTAATTAGGAAATTCAAGTTGGCCAATAATGCAATTCTCTGACATTAA
AAATAATTCTATTCAAATACTGCATATTGATTACACCTCATACTGTGATAATTAA
GATGTGGATTGCTGGTCCAGCATGCCATAAACAGGTAGAAGAATGATGAAATGTT
AGAATAAAACTCTGCTTATAGTACTACACAGTCAAAAGATGTTAAAATGCTTTG
TTACTGCGCATGTAATTGAAATATATAGATTATTGTAACCTTCAACCTGAAAATCAAGCAGT
ATGAGAGTTAGTTATTGTTGATGTCAGTAGTGTCTAATGAAGCTTAAAATCTACATT
TCTTCTTAAAATATTATTAAATGTAATGGAATGAAATAACAAATTGAGCTTAATTCCCCAAC
TTATTCTGTGTAGACATTGTTCCACAATTGAAATGGCTGTGTTACCTCTAAATAA
ATGAATTGAGAAAAAAAAAAAAAA

FIGURE 41

MGSVLGLCSMASWI~~PCLCGSAPCLLCRCCPSGNSTVTRLIYALFLLVGVCVACVMLIPGME~~
~~EQLNKIPGFCENEKGVVPCNILVGYKAVYRLCFGAMFYLLLSSLLMIKVKSSSDPRAAVHNG~~
~~FWFFKFAAAIAIIIGAFFIPEGTFTTVWFYVGMAGAFCFILIQLVLLIDFAHSWNESWVEKM~~
~~EEGNSRCWYAALLSATALNYLLSLVAIVLFFVYYTHPASCSENKAFIGISVNMLLCVGASVMSI~~
~~LPKIQESQPRSGLLQSSVITVYTMYTWSAMTNEPETNCNPSSLSSIIGYNTTSTVPKEGQSV~~
~~QWWHAQGIIGLILFLLCVFYSSIRTSNNSQVNKLTLTSDESTLIEDGGARSDGSLEDGDDVH~~
~~RAVDNERDGVTVSYSSFFHMLFLASLYIMMTLTNWSRYEPSREMKSQWTAVWVKISSSWIGI~~
VLYVWTLVAPLVLTNRDFD

FIGURE 42

GCGAGAAAGCTGTCTCCATCTTGTCTGTATCCCGCTGTTCTGNACGTTGTGGAGAT
GGGGAGCGTCCCTGGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTGTGTGGAAGTGCC
CCGTGTTGCTATGCCGATGCTGTCTAGTGAAACAANTCCACTGTAACTAGATTGATCTA
TGCACCTTCTTGCTTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAG
AACAACTGAATAAGATTCTGGATTTGTGAGAATGAGAAAGGTGTTGTCCCTGTAACATT
TTGGTTGGCTATAAAGCTGTATATCGTTGTGCTTGTTGGCTATGTTCTATCTTCT
CTCTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTCACAATGGAT
TTTGGTTCTTAAATTGCTGCAGCAATTGCAATTATTATTGGGGC

FIGURE 43

GTTATTGTGAACCTTGTGGAGATGGGAGGTCTGGGCTGTGTTCCATGGCGAGCTGGATAAC
CANGTTGTGTGGAAGTGCCCCGTGTTGNTATGCCGATGCTGTCCTAGTGGAAACAANTCC
ACTGTAATTAGATTGATNTATGCACCTTTNTGCTTGGAGTAGTGTAGCTTGTGTAAT
GTTGATACCAGGAATGGAAGAACAACTGAATAAGATTCTGGATTTGTGAGAATGAGAAAG
GTGTTGCCCTTGTAAACATTGGTTGGCTATAAAGCTGTATNGTTGTGCTTGGTTG
GCTANGTTCTATNTTCTTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAG
AGCTGCAGTGCACAATGGATTGGTTTAAATTGCTGCAGCAATTGCAATTATTATTG
GGGC

FIGURE 44

AAGAAGCTGTCTCCATCTTGTCTGTATCCGCTGCTCTGTGAACGTTNTGGAGATGGGGAGC
GTCCTTGGGGTTGTGCTCCATGGCGAGCTGGATACCATGTTGTGTGGAAGTGCCCCGTGTT
TGCTATGCCGATGCTGTCCTAGTGGAAACAACACTCCACTGTAACTAGATTGATCTATGCACTT
TTCTTGCTTGGAGTATGTGTAGCTTGTATAATGTTGATACCAAGGAATGGAAGAACAACT
GAATAAGATTCTGGATTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAAACATTGGTTG
GCTATAAAGCTGTATATCGTTGTGCTTGGCTATGTTCTATCTCTCTCTTTA
CTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTCACAATGGATTTGGTT
CTTAAATTGCTGCAGCAATTGCAATTATTATTGGGGC

FIGURE 45

GCTGTCCTTAGTGGAAACAANTCCAAC TTGTAAC TGATTGATCTATGCAC TTTCCCTTG
CTTGGAGTATGTGAGCTTGTGAATGTTGTTCCAGGATTGGANGAACAACTGAATA
AGATTCTGGATT GTGAGAATGAGAAAGGTGTTGCCCCTGTAAACATTTGGTTGGC
TATAAAGCTGTATATCGTTGTGCTTGGCTATGTTCTATCTTCTCTCTTACT
AATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTCACAATGGATTTGGTTCT
TTAAATTGCTGCAGCAATTGCAATTATTATTGGGGCATTCTCATTCCAGAAGGAAC TTT
ACAAC TGTGGTTATGAGGCATGGCAGGTGCCTTGTTCATCCTCATACAACTAGT
CTTACTTATTGATTTGCACATTGAAATGAATCGTGGTTGAAAAAATGGAAGAAGGGA
ACTCGAGATGTTGGTATGCAGCCTGTTATCAGCTACAGCTCTGAATTATCTGCTGTCTTA
GTTGCTATCGTCCTGTTCTTGTCTACTACACTCATCCAGCCAGTGTTCAGAAAACAAGGC
GTTCATCAGTGTCAACATGCTCCTCTGC GTTGGTGCTTCTGTAAATG

FIGURE 46

CTCGGGCGCGCACAGGCAGCTGGTTGCCCTGCATTGAGCTGGGGTCCGGCCGGCCGGCTCTCCAAT
 GGAAATGTGTGGCTGGAGGGAGCGAGGCTTCGGCAAAGGCAGTCAGTGTTCAGACCGGGCAG
 TCCTGTAAAGCAGATAAAAGAAAACATTATTAACGTGTATTACAGAGGGAGCAGCCGGCCGGGCTGTC
 ACTCCCCCGGAACATTGGCTCCCTCAGCTCCAGAGAGAGGAGAAGAAGAAAAGCGAAAAGAGGAGATT
 GTCGTTCCAGCCAAGTGGACCTGATCGATGCCCTCTGAATTATCACGATATTGATTATTAGCGATGCC
 CCCTGGTTGTGTACGCACACACAGTGACACAAGGCTGGCTCGCTCCCTCGTTCCAGCTCC
 TGGCGAATCCCACATCTGTTCAACTCTCCCGAGGGCAGCAGGAGCAGAGTGTGCAATCGCAGTG
 AAGAGGGACGAGGGAAAAGAAACAAAGCCACAGCACAATTGAGACTCCGCATCCAAAAGAACACCAGAT
 CAGAAAAAGAAGATGGGCCCGAGGCTCGTGTGCTTGCTGTCCGAACCTGTTCTCCCTGCTGG
 TGGAGCTGGCCCTCTGTGACGCCACCCCTGAAAGGCAGGTTACAGAGGACCGCAGGAACATCCGCC
 ACATCATCTGGTGTGACGGACGACCAGGATGTGGAGCTGGGTCCATGCAGGTGATGAACAAGACCCGGCG
 ATCATGGAGCAGGGGGGGCGCACTTCATCACCGCTTCGTGACACACCCATGTGCTGCCCTCACGCTC
 CATCCTCATGGCAAGTACGTCCACAACACCATCACCAACAATGAGAAGTGCCTCTGCCCTGCC
 AGGCACAGCACGAGAGCGCACCTTGGCGTGTACCTAACAGACTGGCTACCGGACAGCTTCTCGGGAA
 TATCTTAATGAATAACACGGCTCTACGTGCCACCCGGCTGAAAGGAGTGGTGGACTCCTTAAAGACTCC
 CTTTATAACTACACGCTGTGCGAACGGGTGAAAGAGAAGCAGGCTCCGACTACTCCAAGGATTACCTCA
 CAGACCTCATACCAATGACAGCTGAGCTTCTCCGACAGTCAAAGAAGATGTACCCGACAGGCAAGTCTC
 ATGGTCACTAGCCATGCAGCCCCACGGCCCTGAGGATTACGCCCCACAATATTACGCCCTTCCAAACGC
 ATCTCAGCACATCACGCCAGCTACAACACTACGCGCCAAACCGGACAAACACTGGATCATGCGTACACGGGG
 CCATGAAGCCCATCCACATGGAATTACCAACATGCTCCAGCGGAAGCGCTGAGACCCCTCATGCGTGGAC
 GACTCCATGGAGACGATTACAACATGCTGGTTGAGACGGCGAGCTGGACAACACGTACATGTATACACC
 CGACCACGGTACCCACATGGCAGTTGGCCTGGTGAAGGGAAATCCATGCCATATGAGTTGACATCAGGG
 TCCCCTCTACGTGAGGGGCCAACGTGAGGCCCTGTCTGAATCCCCACATGCTCTAACATTGACCTG
 GCCCCCACCATCCTGGACATTGAGGCTGGACATACTGCGGATATGGACGGGAAATCCATCCTCAAGCTG
 GGACACGGAGCGCCGGTGAATCGTTTACTGAAAAAGAAGATGAGGGCTGGCGGACTCCTCTGGTGG
 AGAGAGGCAAGCTGACACAAGAGAGACAAGGTGGACGCCAGGAGGAGAACCTCTGCCAAGTAC
 CAGCGTGTGAAGGACCTGTCAGCGTCTGAGTACACAGACGGCGTGTGAGCAGCTGGACAGAAGTGGCAGTG
 TGTGGAGGAGCCACGGGAAGCTGAGCTGACATAAGTGAAGGGCCCATGCGGCTGGCGGAGCAGAGGCC
 TCTCCAACCTGTGCCAACGACTACAGGGCAGGGCAGCGAGGCTGCACCTGTGACAGGGGACTACAAGCTC
 AGCCTGGCCGGACGCCGGAAAAAAACTCTTCAAGAAGAAGTACAAGGCCAGCTATGTCGGCAGTCGCTCCATCG
 CTCAGTGGCCATCGAGGTGGACGGCAGGGTGTACCACTAGGCTGGTGTGCCCCAGCCCCGAAACCTCA
 CCAAGCGGCACTGGCCAGGGCCCTGAGGACCAAGATGACAAGGATGGTGGGACTTCAGTGGCACTGGAGGC
 CTTCCGACTACTCAGCCGCCAACCCATTAAGTGAACACATGGTGTACATCCTAGAGAACGACACAGTCCA
 GTGTGACCTGGGACCTGTACAAGTCCCTGCAGGCCTGAAAGACACAGCTGCACATCGACCGACAGGATTGAA
 CCCTGCAGAACAAAATTAAGAACCTGAGGGAGTCCGAGGTCACCTGAAGAAAAAGCGGCCAGAAGAATGTGAC
 TGTCACAAAATCAGTACCAACACCCAGCACAAGGCCCTCAAGCACAGAGGCTCCAGTCTGATCCTTCAG
 GAAGGGCTGCAAGAGAAGGACAAGGTGTGGCTGTGCGGGAGCAGAAGCAGAAGAAGAAACTCCGCAAGCTGC
 TCAAGCGCCTGCAGAACACGACACGTGCACTGCCAGGCCTCACGTGCTCACCCACGACAACCAGCACTGG
 CAGACGGCCCTTCTGGACACTGGGCCCTTCTGTGCCCTGCACAGCGCAACAAATAACACGTACTGGTGCAT
 GAGGACCATCAATGAGACTCACAATTCTCTCTGTGAATTGCAACTGGCTCCTAGAGTACTTGTATCTCA
 ACACAGACCCCTACCGAGCTGATGAATGCACTGAAACACACTGGACAGGGATCTCCCTAACAGCTACACGTACAG
 CTCATGGAGGCTGAGGAGCTGCAAGGGTACAAGCAGTGTAAACCCGGACTCGAAACATGGACCTGGATGGAGG
 AAGCTATGAGCAATACAGGCAAGTGGAGGTAAAGAAGAGGCTCTTCAACTGCTTCCAAATCACTG
 GACAAGTGGAGGCTGGAGGT**TAA**AAACACAGAGGTGGACCTCCAAAACATAGAGGCATCACCTGA
 CTGCACAGGCAATGAAAACATGTGGGTATTCCAGCAGACCTGTCTATTGGCCAGGAGGCCTGAGAAAGC
 AAGCACGCACCTCACTGACATGACAGATTCTGGAGGATAACCGAGCAGGAGCAGAGATAACTCAGGAAGTCC
 ATTTTGGCCCTGCTTTGCTTGGATTATACCTCACAGCTGCACAAAATGCAATTTCCTGTATCAAAAGTC
 ACCACTAACCCCTCCCCAGAAGCTCACAAAGAAAACGGAGAGAGCGAGCGAGAGAGATTCTTGGAAATTTC
 TCCCAAGGGCGAAAGCTATTGAAATTAAATCATAGGGAAAAGCAGTCTGTCTAAATCCTTATTCTT
 TTGGTTGTACAAAGAAGGACTAAGAACGAGGACAGAGGCAACGTGGAGAGGGCTGAAAACAGTCAGAGACG
 TTTGACAATGAGTCAGTAGCACAAAGAGATGACATTACACTATAAACCTGGTGCCTCTGAAGAAA
 CTGCCTCATTGTATATGTGACTATTACATGAAACATGGAACTTTAGGGAACCTAATAAGAAA
 CCCAATTTCAGGAGTGGTGGTCAATAAACGCTCTGTGGCCAGTGTAAAAGAAAA

FIGURE 47

MGPPSLVLCLLSATVFSLLGGSSAFLSHHRLKGRFQRDRRNIRPNIILVLTDDQDVELGSMQ
VMNKTRRIMEQGGAHFINAFVTTPMCCPSRSSILTGYVHNHNTYTNNECSSPSWQAQHES
RTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWGLLKNSRFYNYTLCRNGVKEKGSD
YSKDYLTDLITNDSVSFFRTSKKMYPHRPVLMVISHAAPHGPEDSAPQYSRLFPNASQHITP
SYNYAPNPDKHWIMRYTGPMPKPIHMEFTNMLQRKRLQTLMVVDDSMETIYNMLVETGELDNT
YIVYTADHGYHIGQFGLVKGKSMPYEFDIRVPFYVRGPNEAGCLNPHIVLNIDLAPTI
AGLDIPADMKGSIKLKDTERPVNRFHLLKKMRVWRDSLVERGKLLHKRDNDKVDAQEEN
FLPKYQRVKDLCQRAEYQTACEQLGQKWQCVEDATGKLKLHKCKGPMRLGGSRALSNLVPKY
YGQGSEACTCDSGDYKLSLAGRRKKLFKKKYKASYVRSRSIRSVAIEVDGRVYHVGLGAAQ
PRNLTKRHWPAGAPEDQDDKDGGDFSGTGGLPDYSAANPIKVTHRCYILENDTVQCDLDLYKS
LQAWKDHKLHIDHEIETLQNKIKNLREVRGHLKKKRPEECDCCHKISYHTQHKGRLHRGSSL
HPFRKGLQEKDVKWLREQRKKKLRKLLKRLQNNDTCSMPGLTCFTHDNQHWQTAPFWTLG
PFCACTSANNNTYWCMTINETHNFLFCEFATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQL
HVQLMELRSCKGYKQCNPTRNMDLDGGSYEQYRQFQRRKWEPMKRPSKSLGQLWEGWEG

FIGURE 48

AACAAAGTCAGTGAUTGAGAGGGCTGAGCGGAGGCTGCTGAAGGGGAGAAAGGAGTGAGGA
GCTGCTGGCAGAGAGGGACTGTCCGGCTCCAG**ATG**CTGGCCTCCTGGGAGCACAGCCC
TCGTGGATGGATCACAGGTGCTGCTGTGGCGGTCTGCTGCTGCTGCTGCTGGCCACC
TGCCTTTCCACGGACGGCAGGACTGTGACGTGGAGAGGAACCGTACAGCTGCAGGGGAAA
CCGAGTCCGCCGGGCCAGCCTGGCCCTCCGGCGGGGCCACCTGGGAATTTCA
ATCACCGTCATCCTGGCCACGTATCTCATGTGCCAATGTGGCCTCCACCACCAC
CCCCGCCACACCCCTACCAACCTCCACCACCACCCACCGCCACCATCCCCGCCA
CGCTCGC**TGA**GGCTGCTGTCGCCGGTGCCTGTGGACAGCAGCTGCCCTGCCCTCCATCTG
TTCCCAGGACAAGTGGACCCATGTTCCATGTGGAAGGATGCATCTCTGGGTGAACGAGG
GGAACAATAGACTGGGGCTTGCTCCAGCTGCATTGCATGGCATGCCCTGGTACTATGGC
AGCAGAGAATGGAGGAACACTGGGTCTGCAGTGCTGAAGGGTTGGGAGTGGAGAGCAAGG
GTGCTTTGGGGCTGGACAGCCGTCTTGACAGTGACTCCAGTGAGCCCCAGAAATG
ACAAGCGTGTCTGGCAGGCCAGCACACAAGTGGATGTGAAGTGCCGTCTGACCTCCTC
ATCAGGCTGCTGCAGGCCTCTGGCGGGCAGGGCACTGGGAGAGGCCCTGAGAATGTCCTTT
GGTTGGAGAAGGCAGTGTGAGGCTGCACAGTCAATTGACGGTGCCTAGTCCAAGAAAAT
AAAAACCACTAAGAAGCTTAAAAAAAAAAAAAAA

FIGURE 49

MLGLLGSTALVGWITGAAVAVLLLLLTLATCLFHGRQDCDVERNRTAAGGNVRRAQPWPFR
RRGHLGIFHHHRHPGHVSHVPNVGLHHHHPRHTPHHLHHHHPRHHPRHAR

FIGURE 50

GGC GGCTG CTGAGCTGC CTTGAGGTGCAGT GTTGGGGATCCAGAGCC **ATG** TCGGACCTGCTA
 CTACTGGGCCTGATTGGGGCCTGACTCTTACTGCTGCTGACGCTGCTGGCCTTGCCGG
 GTACTCAGGGCTACTGGCTGGGTGGAAGTGAGTGCTGGTCACCCCCCATCCGAAACGTCA
 CTGTGGCCTACAAGTTCCACATGGGCTCTATGGTGAGACTGGCGGCTTTCACTGAGAGC
 TGCAGCATCTCTCCAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCCCACATGGTGCC
 CCCTGATAAGTGCCGATGTGCCGTGGCAGCATTGAGTGAAAGGTGAGGAATGCCCTCCC
 CTGAGCTCATCGACCTCTACCAGAAATTGGCTCAAGGTGTTCTCCTCCGGCACCCAGC
 CATGTGGTGACAGCCACCTTCCCCTACACCACCATCTGTCCATCTGGCTGGCTACCCGCCG
 TGTCCATCCTGCCTGGACACCTACATCAAGGAGCGGAAGCTGTGCTATCCTCGGCTGG
 AGATCTACCAGGAAGACCAAGATCCATTTCATGTGCCACTGGCACGGCAGGGAGACTTCTAT
 GTGCCCTGAGATGAAGGAGACAGAGTGAAATGGCGGGGCTTGTGGAGGCCATTGACACCCA
 GGTGGATGGCACAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGGAAAGTGAGCC
 CTGGCAGCCGGAGACTTCAGCTGCCACACTGTCACCTGGCGAGCAGCCGTGGCTGGGAT
 GACGGTGACACCCGCAGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGCTCCTTTGA
 GGAGCTGGACTTGGAGGGCGAGGGGCCCTAGGGGAGTCACGGCTGGACCCCTGGACTGAGC
 CCCTGGGACTACCAAGTGGCTCTGGAGGCCACTGCCCTGAGAAGGGCAAGGAG**TAA**CCC
 ATGGCCTGCACCCCTCCTGCAGTGCAGTTGCTGAGGAAC TGAGCAGACTCTCCAGCAGACTCT
 CCAGCCCTTCCCTCCTCTGGGGAGGAGGGGTTCTGAGGGACCTGACTTCCCTG
 TCCAGGCCCTTGCTAAGCCTCTCCTCACTGCCCTTAGGCTCCAGGGCCAGAGGAGCCA
 GGGACTATTTCTGCACCAGCCCCAGGGCTGCCGCCCTGTTGTCTTTTCAGACTC
 ACAGTGGAGCTTCAGGACCCAGAATAAGCCAATGATTTACTGTTCACCTGGAAAAAAA
 AAAAAAAA

FIGURE 51

MSDLLLGLIGGLTLLLLLTLAFAAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGLYGETGR
LFTESCSISPRLRSIAVYYDNPHMVPDKCRCAVGSILSEGEESPSPLEIDLQKFGFKVFS
FPAPSHVVTATFPYTTILSIWLATRRVHPALDTYIKERKLCAYPRLEIYQEDQIHFMCPALAR
QGDFYVPEMKETEWKWRGLVEAIDTQVDGTGADTMSDTSSVSLEVSPGSRETSAAATLSPGAS
SRGWDDGDTRSEHSYSESAGSSFEELDLEGEGPLGESRLDPGTEPLGTTKWLWEPTAPEK
GKE

FIGURE 52

CCGCGGGAACGCTGTCTGGCTGCCGCCACCGAACAGCCTGTCCTGGTGC
CCCCCGCGCCCAGTCATGACCCTGCGCCCTCACTCCTCCGCTCCATCTGCTGCTGCT
GCTGCTCAGTGC CGCGGTGTGCCGGCTGAGGCTGGCTCGAAACCGAAAGTCCC
GTCCGAAACTGGAGACCTGGTGGAGCCCCAGAACCATGTGCCGAGCCC
GTGCTTGGTAGATGGACGTATTATTGACACCTCCCT
GACACGCTTCACATACACTACACGGGAAGCTGGTAGATGGACGTATT
GACACCTCCCT
GACCAGAGACCCCTGGTTATAGAACTTGGCAAAAGCAGGTGATT
CCAGGTCTGGAGCAG
GAGCTGGTAGATGGACGTATT
GGCTTCTCGACATGTGTGGAGAGAACGCAAGGGCAATCAT
TCCTCTCACTTGGCCTAT
GGAAAACGGGATTCCACCATCTG
TCCCAGCGGATGCAGTGGTAGATGACGTGGAGCT
GATTGCACTAATCCGAGCCA
ACTACTGGCTAAAGCTGGTAGAGGGCATT
TGCCTCTGGTAG
GGATGGCCATGGTGCCAGCCCTCCTGGGCTCATTGGTAG
ACCTATA
CAGAAAGGCCAAT
AGACCCAAAGTCTCCAAAAAGAAGCTCAAGGAAGAGAA
ACGAAACAAGAGCAAAAGAAATA
ATAAATAATAAATTTAAAAAACTTAAAAAAAAAAAAAA

FIGURE 53

MTLRPSLLPLHLLLLLSSAAVCRAEAGLETESPVRTLQVETLVEPPEPCAEPAAFGDTLHI
HYTGSIVDGRIIDTSLTRDPLVIELGQKQVIPGLEQSILDMCVGEKRRAIIPSHLAYGKRGF
PPSVPADAVVQYDVELIALIRANYWLKVKGILPLVGMAMVPALLGLIGYHLYRKANRPKVS
KKKLKEEKRNKSKKK

FIGURE 54

CCCGGGAACGTGTTCTGGCTGCCGCACCGAACAGCCTGTCCTGGTGCCCCGGCTCCCTGC
CCCGCGCCCAGTCATGACCCTGCGCCCCCTCACTCCTCCGCTCCATCTGCTGCTGCTGCTGC
TGCTCAGTGCAGGGCTGAGGCTGGCTCGAAACCGAAAGTCCGTCCGGACC
CTCCAAGTGGAGACCCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTGGAGA
CACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCTGA
CCAGAGACCCTCTGGTTATAGAACTGGCAAAAGCAGGTGATTCCAGGTCTGGAGCAGAGT
CTTCTCGACATGTGTGGAGAGAACGCAAGGGCAATCATTCCCTCTCACTTGGCCTATGG
AAAACGGGATTCCACCATCTGTCCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCTGA
TTGCACTAATCCGAGCCAACTAAGCTGGCTAAAGCTGGTAAGGGCATTTCGCCTCTGGTAGGG
ATGGCCATGGTGCCACCCCTCTGGGCTCATTGGGTATCACCTATAACAGAAAGGCCAATAGA
CCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAGAAATAATA
ATAATAAATTTAAAAAACTTA

FIGURE 55

CCGAAAGTCCCCTCCGGACCCCTCCAAGTGGAGACCCCTGGTGGAGCCCCAGAACCATGTGCC
GAGCCCGCTGCTTTGGAGACACGCTTCACATACACTACACGGGAAGCTGGTAGATGGACG
TATTATTGACACCTCCCTGACCAGAGACCCCTGGTTATAGAACTTGGCAAAAGCAGGTGA
TTCCAGGTCTGGAGCAGAGTCTTCTCGACATGTGTGGAGAGAAGCGAAGGGCAATCATT
CCTTCTCACTTGGCCTATGAAAACGGGGATTCCACCATCTGTCCCAGCGGATGCAGTGTT
GCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAACTAAGCTGGCTAAAGCTGGTAAGG
GCATTTGCCTCTGGTAGGGATGCCATGGTGCCAGCCCTCTGGCCTCATTGGGTATCAC
CTATACAGAAAGGCCAATAGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAACGAAA
CAAGAGCAAAAGAAATAATAATAATAATTTAAAAACTTAAAA

FIGURE 56

CTGCTGCATCCGGGTGTCGGAGGCTGTGGCCGTTTGGCTAAATCGGGGAG
 TGAGGCAGGCCGGCGCGACACCAGGCTCCGAACCACTGCACGACGGGCTGGACTG
 ACCTGAAAAAA**ATG**TCTGGATTCTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGG
 GAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTACTATTTTACAGGCTGGTGGAT
 TATCATAGATGCAGCTGTTATTATCCCACCATGAAAGATTCAACCACTCATACCATGCCT
 GTGGTGTATAGCAACCATAGCCTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGA
 GGTGATAGTTACAGTGAAGGTTGTCGGTCAAACAGGTGCTCGCATTGGCTTCGTTGG
 TTTCATGTTGGCCTTGGATCTCTGATTGCATCTATGGATTCTTTGGAGGTTATGTTG
 CTAAAGAAAAAGACATAGTATAACCTGGAATTGCTGTATTCCAGAATGCCTCATCTT
 TTTGGAGGGCTGGTTTAAGTTGGCCGACTGAAGACTTATGGCAG**TGA**ACACATCTGAT
 TTCCCACAGCACAAACAGCCCTGCATGGTTGTTTACTGCTCACTCCAACCTT
 TTGTAATGCCATTCTAAACTTATTCGAGTGTAGTCTCAGCTAAAGTTGTGTAATACT
 AAAATCACGAGAACACCTAAACAACAAACAAAAATCTATTGGTATGCACTTGATTAACCT
 ATAAAATGTTAGAGGAAACTTCACATGAATAATTTGTCAAATTTATCATGGTATAATT
 TGTAAAAATAAAAGAAATTACAAAGAAATTATGGATTGTCAATGTAAGTATTGTCATA
 TCTGAGGTCAAACACAATGAAAGTGCTCTGAAGATTAAATGTGTTATTCAAATGTGGT
 CTCTTCTGTGTCATGTTAAATGAAATATAACATTAGTTTAAATATTCCGTGG
 TCAAAATTCTCCTCACTATAATTGGTATTACCAAAATTCTGTGAACATGTAAT
 GTAACTGGCTTGAGGGCTCCAAAGGGTGAGTGGACGTGTTGGAAGAGAGAACCAT
 GGTCCAGCCACCAGGCTCCCTGTGTCCTCATGGGAAGGTCTCCGCTGTGCCTCTCATT
 CCAAGGGCAGGAAGATGTGACTCAGCCATGACACGTGGTTCTGGTGGATGCACAGTCAC
 CACATCCACCACTG

FIGURE 57

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFTGWIIIDAIVYPTMKDFNHSYHACGVI
ATIAFLMINAVSNGQVRGDSYSEGCLGQTGARIWLFGFMLAFGSLIASMWILFGGYVAKER
DIVYPGIAVFFQNAFIFFGGLVFKFGRTEDLWQ

FIGURE 58

TTCTTGGCTAAAATCGGGGGAGTGAGGC GGCGCGCGACACCGGGCTCCGGAACC
ACTGCACGACGGGGCTGGACTGACCTGAAAAAAATGTCTGGATTCTAGAGGGCTTGAGATG
CTCAGAATGCATTGACTGGGGGAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTAC
TATTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGAT
TTCAACCACTCATACCATGCCTGTGGTGTATAGCAACCATAGCCTCCTAATGATTAATGC
AGTATCGAACATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTGTCTGGTCAAACAGGTG
CTCGCATTGGCTTTCGTTGGTTCATGTTGGCCTTGGATCTCTGATTGCATCTATGTGG
ATTCTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATT
TTTCCAGAACATGCCTTCATCTTTGGAGGGCTGGTTTAAGTTGGC

FIGURE 59

TGGACGGACCTGAAAAAAATGTTGGATTNTAGAGGGNTTGAGATGTTCAGAATGCATGAC
TGGGGAAAAGCGCAAATACTATTGCTTCATTGCTGCTGGTGTANTATTTTACAGGCTG
GTGGATTATCATAGATGCAGNTGTATTATCCCACCATGAAAGATTCAACCANTCATACC
ATGCCTGTGGTGTATAGCAACCATAGCCTCNTAATGATTAATGCAGTATCGAATGGACAA
GTCCGAGGTGATAGTTACAGTGAAGGTTGTTGGGTCAAACAGGTGCTCGCATTGGCTTT
CGTTGGTTCATGTTGGCCTTGGATCTCTGATTGCATCTATGTGGATTCTTTGGAGGTT
ATGTTGCTAAAGAAAAAGACATAGTATAACCTGGAATTGNTGTATTTTCCAGAATGCCTTC
ATCTTTTGGAGGGCTGGTTTAAGTTGGCCGACTGAAGANTTATGGCAGTG

FIGURE 60

GGACACCGGGTCCGGACCAATGCANGACGGGTGGANTGACCTGAAAAAAATGTTGGATT
TTTAGAGGGCTTGAGATGNTCAGAATGCATTGACTGGGGAAAAGCGCAATANTATTGCTTT
CCATTGCTGCTGGTGTACTATTTTACAGGGTGGATTATCATAGATGCAGCTGTTATT
TATCCCACCATGAAAGATTNAACCACTCATACCATGCCTGTGGTGTATAGCAACCATAGC
CTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTT
GTTTGGGTCAAACAGGTGNTCGCATTGGCTTCGTTGGTTCATGTTGGCCTTGGATTT
CTGATTGNATTCTATCGGGATTCTTCTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTAT
ACCCTGGAATTNCTNTATTTTCCAGAATGCC

FIGURE 61

TAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTCC
ATTGNTGNTGGTGTANTATTTTACAGGCTGGTGGATTATNATAGATGCAGCTGTTATTT
ATCCCACCATGAAAGATTNAACCANTCATACCATGCCTGTGGTGTATAGCAACCATAGCC
TTCCTAATGATTAATGCAGTATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG
TTTGGGTCAAACAGGTGNTNGCATTGGCTTNAGTGGTTCATGTTGGCCTTGGATCTN
TGATTGCATTTATGTGGATTNTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAAC
CCTGT

FIGURE 62

GGGAGGCCTGTGNCCGTTGTTNTGGCTAAAATCGGGGGAGTGAGGC GGCCC GGCG CG
CGNGACACCGGGTCCGGGAACCATTGCACGACGGGTGGACTGACCTGAAAAAAATGTTG
GATTTNTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATT
GCTTCCATTGCTGCTGGTGTACTATTTTACAGGCTGGTGGATTATCATAGATGCAGCTGT
TATTTATCCCACCATGAAAGATTCAACCACTCATACCATGCCTGTGGTGTATAGCAACCA
TAGCCTTCCTAACATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAA
GGTTGTCTGGTCAAACAGGTGCTCGCATTGGCTTTCGTTGGTTCATGTTGCCCTTGG
ATNTCTGATTGCATCTATGTGGATTCTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAG
TATACCCCTGGAATTGCTGTATTTCCAGAATGCCTCATNTTTTGGAGGGCTG

FIGURE 63

CGACGCCGGCGT**ATGT**GGCTCCGCTGGTGCCTGGCTGTGCTGCTGGCCGTCC
 TCTGCAAAGTTACTTGGGACTATTCTCTGGCAGCTCCCAGAACCTTCTCCGAAGATGTC
 AACCGGCCCGAGGCCCTGGTAAGTGACAAGGAGGCCAGGAAGAAGGTTCTCAAACAAGC
 TTTTCAGCCAACCAAGTGCCGGAGAAGCTGGATGTGGTGTAAATTGGCAGTGGCTTGGG
 GCCTGGCTGCAGCTGAATTCTAGCTAAAGCTGGCAAGCGAGCTGGCTGGCTGGAAACAACAT
 ACCAAGGCAGGGGGCTGCTGTCACTACCTTGGAAAGAATGGCCTTGAATTGACACAGGAAT
 CCATTACATTGGCGTATGGAAGAGGGCAGCATGGCGTTTATCTGGACCAGATCACTG
 AAGGGCAGCTGGACTGGGCTCCCCCTGTCCTCCTTGTACATCATGGTACTGGAAGGGCCC
 ATGGCCGAAAGGAGTACCCATGTACAGTGGAGAGAAAGCCTACATTAGGGCCTCAAGGA
 GAAGTTCCACAGGAGGAAGCTATCATTGACAAGTATAAAGCTGGTTAAGGTGGTATCCA
 GTGGAGCCCCATGCCATCTGTTGAAATTCCCTCCATTGCCGTGGTCAAGCTCCTCGAC
 AGGTGTGGCTGCTGACTCGTTCTCCATTCTCAAGCATCCACCCAGAGCCTGGCTGA
 GGTCTGAGCAGCTGGGGCCTCTGAGCTCCAGGCAGTACTCAGCTACATCTCCCCA
 CTTACGGTGTACCCCCAACACAGTGCCTTCCATGCACGCCCTGCTGGTCAACCAACTAC
 ATGAAAGGAGGCTTTATCCCCGAGGGGGTCCAGTGAATTGCCTCCACACCATTCCCTGT
 GATTCAAGCGGGCTGGGGCGCTGCTCACAAGGCCACTGTGCAGAGTGTGTTGCTGGACT
 CAGCTGGAAAGCCTGTGGTGTCAAGTGTGAAGAAGGGGCATGAGCTGGTGAACATCTATTG
 CCCATCGGGCTCCAACCGCAGGACTGTTCAACACCTATGAACACCTACTGCCGGGGAACGC
 CCGCTGCCAGGTGTGAAGCAGCACTGGGGACGGTGCGGGCCGGCTTAGGCATGACCT
 CTGTTTCACTGCCCTGCGAGGCACCAAGGAAGACCTGCATCTGCCGTCCACCAACTACTAT
 GTTACTATGACACGGACATGGACCAGGCGATGGAGCGCTACGTCTCCATGCCAGGGAAAGA
 GGCTGCCAACACATCCCTCTCTCGCTTCCATCAGCAAAGATCCGACCTGGG
 AGGACCGATTCCCAGGCCGGTCCACCATGATCATGCTCATACCAACTGCCTACGAGTGGTT
 GAGGAGTGGCAGGGAGCTGAAGGGAAAGCAGGGCAGTGACTATGAGACCTTAAAAACTC
 CTTGTGGAAGCCTTATGTCAGTGGTCTGAAACTGTTCCACAGCTGGAGGGAAAGGTGG
 AGAGTGTGACTGCAGGATCCCCACTCACCAACCAGTTCTATCTGGCTGCTCCCCGAGGTGCC
 TGCTACGGGGCTGACCATGACCTGGGCCGCTGCACCCCTGTGTGATGCCCTCCTTGAGGGC
 CCAGAGCCCCATCCCCAACCTCTATGACAGGCCAGGATATCTCACCTGTGGACTGGTCG
 GGGCCCTGCAAGGTGCCCTGTCAGCAGGCCATCTGAAGCAGGAACCTGTACTCAGAC
 CTTAAGAATCTGATTCTAGGATCCGGGACAGAAGAAAAAGAAAT**TAG**TTCCATCAGGGAGG
 AGTCAGAGGAATTGCCAATGGCTGGGCATCTCCCTGACTTACCCATAATGTCTTCTG
 CATTAGTTCTGCACGTATAAGCACTCTAATTGTTCTGATGCCTGAAGAGAGGCCCTAG
 TTTAAATCACAATTCCGAATCTGGGCATGGAATCACTGCTCCAGCTGGGCAGGTGAGA
 TCTTACGCCTTTATAACATGCCATCCCTACTAATAGGATATTGACTGGATAGCTTGATG
 TCTCATGACGAGCGCGCTCTGCATCCCTACCCATGCCTCTAACACTCAGTGATCAAAGCGA
 ATATTCCATCTGTTGAGAACCCCTGGCAGTGTGTCAGCTCAACCTGGTGGGTTCAAGTC
 TGTCCTGAGGCTCTGCTCTCATTCTAGTGCAGCTGCACAGTTCTACACTGTCAAGG
 GAAAAGGGAGACTAATGAGGCTTAACTCAAAACCTGGCGTGGTTGGTGCATTCCATA
 GGTTGGAGAGCTAGATCTCTTGTGCTGGGTTCAAGTGGCTCTCAGGGACAGGAAT
 GCCTGTGCTGGCAGTGTGGTCTGGAGCTTGGGTAACAGCAGGATCCATCAGTTAGTA
 GGGTGCATGTCAGATGATCATATCCAATTCTATGGAAAGTCCGGGTCTGTCTCCATTATCA
 TCGGGGTGGCAGCTGGTCTCAATGTGCCAGCAGGGACTCAGTACCTGAGCCTCAATCAAGC
 CTTATCCACCAAAACACAGGGAAAGGGTGATGCAGGGAAAGGGTGAACATCAGGAGTCAGGGCA
 TGGACTGGTAAGATGAATACTTGCTGGGCTGAAGCAGGCTGCAGGGCATTCCAGCCAAGGG
 CACAGCAGGGACAGTGCAGGGAGGTGTGGGTAAGGGAGGGAAAGTCACATCAGAAAAGGG
 AAGCCACGGAATGTGTGAAGGCCAGAAATGGCATTGCAAGTTGAAAGTGTGAGGG
 TTAGACAGGTAGGTGAATGCAAGCTCAAGGTTGAAAGTGTGAGTTAGTCAACATTAATAAATTATG
 GTATCAGACATACGAAAGGTCTCTTGTAGTTGTTAATGTAACATTAATAAATTATG
 ATTCCATTGCTTAAAAAAAAAAAAAA

FIGURE 64

MWLPLVLLLAVLLAVLCKVYLGLFSGSSPNPFSEDVKRPPAPLVTDEARKVLKQAFSAN
QVPEKLDVVVIGSGFGGLAAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNGLEFDTGIHYIG
RMEEGSIGRFILDQITEGOLDWAPLSSPFDIMVLEGPNRKEYPMYSGEKAYIQGLKEKFPO
EEAIIDKYIKLVVVSSGAPHAILLKFLPLPVVQLLDRCGLLRFSPFLQASTQSLAEVLQQ
LGASSELQAVLSYIFPTYGVTPNHSAFSMHALLVNHYMKGGFYPRGGSSEIAFHТИPVIQRA
GGAVLTKATVQSVLDSAGKACGVSVKGHELVNIYCIVVSNAGLFNTYEHLLPGNARCLP
GVKQQLGTVRPGLGMTSVFICLRGTKEDLHLPSTNYYVYDTDMDQAMERYVSMPREEAAEH
IPLLFFAFPSAKDPTWEDRFPGRSTMIMLIPTAYEWFEEWQAEKGKRGSDYETFKNSFVEA
SMSVVLKLFQLEGKVESVTAGSPLTNQFYLAAPRGACYGADHDLGRLHPCVMASLRAQSPI
PNLYLTGQDIFTCGLVGALQGALLCSSAILKRNLYSDLKNLDSRIRAQKKKN

FIGURE 65

FIGURE 66

MRVRIGLTLLLCAVLLSLASASSDEEGSQDES LDSKTT LTSDESVKDHTAGR VVAGQIFLD
SEESELESSIQEEEDSLKSQE GE SVTEDISFLES PN PEN K DYEEPKKVRKP ALTAIEGTAH G
EPCHFPFLFLDKEYDECTS D GRED GRLWCATTYDYKADEKWGF C EEEAKRRQM QEAEMM
YQTGMKILNGSNKKSQKREAYRYLQKAASMNHTKALER VS YALLFGDYL P QNIQAAREMFEK
LTEEGSPKGQTALGFLYASGLGVNSSQAKALVYYT F GALGGNLIAHMVLVSRL

FIGURE 67

CTTCCCAGCCCTGTGCCCAAAGCACCTGGAGCATATAGCCTGCAGAACTTCTACTTGCCT
GCCTCCCTGCCTCTGGCC**ATG**GCCTGCCGGTGCCTCAGCTCCTCTGATGGGGACCTCCT
GTCAGTTCCCAGACAGTCCTGGCCAGCTGGATGCACTGCTGGCTTCCCAGGCCAAGTGG
CTCAACTCTCCTGCACGCTCAGCCCCAGCACGTACCACAGGGACTACGGTGTGCCTGG
TACCAGCAGCGGGCAGGCAGTGCCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCA
CCACCGGCCTGCTGACATCCCCGATCGATTCTCGCAGCCAAGGATGAGGCCACAATGCCT
GTGTCCTCACCATTAGTCCC GTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGC
TACGGCTTAGTCCC**TAG**GGGTGGGTGTGAGATGGGTGCCTCCCTCTGCCTCCATTCT
GCCCTGACCTTGGTCCCTTTAAACTTCTCTGAGCCTGCTCCCTCTGTAAAATGGG
TTAATAATATTCAACATGTCAACAAAC

FIGURE 68

MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPQVAQLSCTLSPQHVTIRDYGVSWYQQRAG
SAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPQPEDDADYYCSVGYGFSP

FIGURE 69

GCCGCCCGCCCCGAGACGGGCGGGGGCGCGGGATGC GGCGCCCGGGCG
 CGATGACCGCGGAGCGCACGCCGCGGGCCCTGACCCCGCCGCCGTGAGCCC
 CCCGCCGAGGTCCGGACAGGCCGAGATGACGCCGAGCCCCCTGTTGCTGCTCCTGCTGCCGC
 CGCTGCTGCTGGGGCCTTCCCACCGGCCGCCGCCGAGGCCCAAAGATGGCGGAC
 AAGGTGGTCCCACGGCAGGTGGCCGGCTGGGCCGACTGTGCGGCTGCAGTGCCAGTGGGA
 GGGGACCCGCCGCGCTGACCATGTGGACCAAGGATGGCCGACCATCCACAGCGGCTGGGA
 GCGCTTCGCGTGCTGCCGAGGGCTGAAGGTGAAGCAGGTGGAGCGGGAGGATGCCGGC
 GTGTACGTGTGCAAGGCCACCAACGGCTTCCGAGCCTGAGCCTAAGTACACCCCTGTCGT
 GCTGGATGACATTAGCCCAGGGAAAGGAGAGCCTGGGCCGACAGCTCTCTGGGGGTCAAG
 AGGACCCGCCAGCAGCAGTGGGACGACGCCCTCACACAGCCCTCAAGATGAGGC
 CCGGTGATCGCACGGCCCTGGGTAGCTCCGTGCGCTCAAGTGCCTGGGCCAGCGGGCACCC
 TCGGCCGACATCACGTGGATGAAGGACGACAGGCCCTGACCGGCCAGAGGCCGCTGAGC
 CCAGGAAGAAGAAGTGGACACTGAGCCTGAAGAACCTGCGGCCGGAGGACAGCGGCAAATAC
 ACCTGCCCGTGTGAAACCGCGCGGCCATCAACGCCACCTACAAGGTGGATGTGATCCA
 GCGGACCGTTCAAGCCGTGTCACAGGACGCAACCGCTGAACACGACGGTGGACTTCG
 GGGGACACGTCCTCCAGTGAAGGTGCCGAGCAGTGAAGCCGGTGAATCCAGTGGCTG
 AAGCGCGTGGAGTACGGCGCGAGGGCCGACAACCTACCATCGATGTGGCGGCCAGAA
 GTTGTGGTGTGCCCCACGGGTGACGTGTGGTCGCGGCCGACGGCTCTACCTCAATAAGC
 TGCTCATCACCCGTGCCGCCAGGACGATGCGGGCATGTACATCTGCCCTGGCGCCAACACC
 ATGGGCTACAGCTCCGAGCGCCTCCACCGTGTGCGAGCAGACGGCCAGGGCC
 ACCTGTGGCTCTCGCCACTAGCCTGCCGTGGCTGGCCCTGGTATCGGCATCCCCAG
 CCGCGCGTGTCTCATCTGGCACCCCTGCTCTGTGGCTTGGCCAGGCCAGAACAGCC
 TGCACCCCGCGCTGCCCTCCCTGCGCTGGCACCGCCGGGGACGGCCCGACCG
 CAGCGGAGACAAGGACCTCCCTCGTTGGCCGCCCTAGCGCTGGCCCTGGTGTGGGCTGT
 GTGAGGAGCATGGTCTCCGGAGCCCCCAGCACTACTGGCCCAGGCCAGTTGCTGGC
 CCTAAGTTGTAACCAAACCTACACAGACATCCACACACACACACACTCTCACAC
 ACACACTACACGTGGAGGGCAAGGTCCACCAGCACATCCACTATCAGTGCTAGACGGCACCGT
 ATCTGCACTGGGACAGGGGGCCCGCCAGACAGGCAACTGGGAGGATGGAGGACGGAGCT
 GCAGACGAAGGCAAGGGACCCATGGCGAGGAGGAATGGCCAGCACCCAGGCAGTCTGTGTG
 TGAGGCATAGCCCTGGACACACACAGACACACACACTACCTGGATGCAATGCA
 ACACATGCGCGCACACGTGCTCCCTGAAGGCACACGTACGCACACGCACATGCACAGATATG
 CCGCTGGCACACAGATAAGCTGCCAAATGCAACGCACAGCACAGAGACATGCCAGAAC
 TACAAGGACATGCTGCCTGAACATACACACCGCACACCCATGCGCAGATGTGCTGCCTGGACA
 CACACACACACGGATATGCTGTCGGACGCACACAGTGCAGATATGGTATCCGGACACA
 CACGTGCACAGATATGCTGCCTGGACACACAGATAATGCTGCCCTGACACACACATGCACGG
 ATATTGCCCTGGAC
 ACATGCAAGATATGCTGCCCTGGACACACACTTCCAGACACACAGTGCACAGGCAGATATGCT
 GCCTGGACACACGCAGATATGCTGCTAGTCACACACACACGCAGACATGCTGCCGGACAC
 ACACACGCATGCACAGATATGCTGTCGGACACACACACACAGCAGCAGATATGCTGCCCTGGAC
 ACACACACAGATAATGCTGCCCTCACACTCACACACAGTGCAGATATTGCCCTGGACACACACA
 TGTGCACAGATATGCTGTCGGACATGCACACACAGTGCAGATATGCTGCCGGATACACAG
 CACGCACACATGCAGATATGCTGCCCTGGCACACACTTCCGGACACACATGCACACACAGGT
 GCAGATATGCTGCCCTGGACACACACAGATAATGCTGCCCTAACACTCACACACAGTGCAGA
 TATTGCCCTGGACACACACATGTGCACAGATATGCTGTCGGACATGCACACACAGTGCAGATA
 TGCTGTCGGATACACACAGCAGCAGATATGCTGCCCTGGCACACACTTCCGG
 CACACATGCACACACAGGTGCAGATATGCTGCCCTGGACACACAGCAGACTGACGTGCTTTGG
 GAGGGGTGTCGCGTGAAGCCTGCACTGAGTACGTGTCGGTGGAGGCTCATAGTTGATGAGGGACTTT
 CCCTGCTCCACCGTCACTCCCCAAGTCTGCCCTGCCCTGCTGCCCTGGGGCTCAGTCCCCGCC
 CATCCCCGCCCTGCTCCCTGGCCCTGGCGCTATTGGCCACCTGCCCTGGGTGCCAGG
 AGTCCCCCTACTGCTGTCGGCTGGGGCTGGGGTGGGGCACAGCAGCCCCAAGCCTGAGAGGCTGGAG
 CCCATGGCTAGTGGCTCATCCCCAGTGCATTCCTCCCCCTGACACAGAGAAGGGGCTTGGTA
 TTTATATTAAAGAAATGAAGATAATTAATAATGATGAGGAAAGGAAAGACTGGGTTGCAAGGGAC
 TGTGGTCTCCCTGGGGCCCGGGACCCGCCCTGGTCTTCAGCCATGCTGATGACCACACCC
 GTCCAGGCCAGACACCACCCCCACCCACTGCTGTTGGCCCCAGATCTCTGTAATT
 TGTAGAGTTGAGCTGAAGCCCCGTATATTAAACACACAAAA

FIGURE 70

MTPSPLLLLLPPLLGAFFPAAAARGPPKADKVVPRQVARLGRTVRLQCPVEGDPPPLTM
WTKDGRTIHSGWSRFRVLPQGLKVQVEREDAGVYVCKATNGFGSLSVNYTLVVLDDISPGK
ESLGPDSSSGQEDPASQQWARPRFTQPSKMRRVIARPVGSSVRLKCVASGHPRPDITWMK
DDQALTRPEAAEPRKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQRTRSKPVL
TGTHPVNTTVDFGGTTSFQCKVRS DVKPVIQWLKRVEYGAEGRHNSTIDVGGQKFVVLPTGD
VWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLTVPDPKPPGPPVASSSSA
TSLPWVIVIGIPAGAVFILGTLLWLCQAQKKPCTPAPAPPLPGHRPPGTARDRSGDKDLPS
LAALSAGPGVGLCEEHGSPAAPQHLLGP GPVAGPKLYPKLYTDIHTHTHSHTHVEGKV
HQHIHYQC

FIGURE 71

CCCAGCTGAGGAGCCCTGCTAAGACACGGTCACTGGATCTGAGAAACTTCCAGGGGACCGCATTCAGAGTC
 AGTGACTCTGTGAAGCACCCACATCTACCTCTGCCACGTTCCCACGGCTGGGGAAAGATGGTGGGGACCA
 AGGCCTGGGTGTTCTCCCTGGTCTGGAAGTCACATCTGTGTTGGGGAGACAGACAGATGCTCACCCAGTCA
 GTAACAAGAGTCCACCCCTGGAGAAGAACCCCAGCATCTTGCACAGGGCAGACTATGAGCGGTGGACGCCATTGCTGG
 TGAGTGGACAACATGGTCAACATCGACTACCCAGGGGGAGGGCAGACTATGAGCGGTGGACGCCATTGCT
 TCTACTATGGGACCGTGTATGCCCCGCCCCCTGCGGCTAGAGGCTGGACCCTGACTGGACACCTGCGGGC
 AGCACTGGCCAGGTGGTCCATGTTAGTCCCCGAGGGCTGGCTCAACAGGGAGCAGCGGCCTGGCCA
 GAACGTGCTTAATTACACCGTACGCTCAGCTGCCCTCTGCCACCAGGATGGCCGGAGACACAGAGCAGCATTGGA
 GCCCATGGTCTCCCTGGAGCAAGTGCTCAGCTGCCCTGGTCAAGACTGGGTCAGACTCGCACACGCAATTG
 TTGGCAGAGATGGTGTGCTGTGCACTGGAGGGCAGCGAAGAGGGTCAAGACTGCATGGGCCAGGACTGTACAGC
 CTGTGACCTGACCTGCCAATGGGCCAGGTGAATGCTGACTGTGATGCTGCATGTGCCAGGACTCTGCTTC
 ATGGGGCTGTCTCCCTGGAGGGCTGGCCCTAGGGCTGCTACCTCTGACCAAGAGACGCCGAAG
 CTGCTGACCCAGACAGACAGTGTGATGGGAGATTCCGAATCCCTGCTGCTGCTGATGCCAAAAGCATCTGAA
 GATCACAAAGGTCAAGTTGCCCCATTGACTCACAATGCCAAGACTAGCCTGAAGGCAGCCACCATCAAGG
 CAGAGTTGTGAGGGCAGAGACTCCATACTGGTGTGAACCTGAGACAAAAGCACGGAGAGCTGGCAGAGC
 GTGTCCTGTGCTGTGAGGGCAGAGCTCCATACTGGTGTGAACCTGAGACAAAAGCACGGAGAGCTGGCAGAGC
 GGATCCTCCCTCAACAGCATGAGGCAAGCTGGTGTGAGGAAACTGCAAGCAGCACCAGGCTGGGAGTACT
 TTTGCAAGGCCAGAGTGATGCTGGGCTGTGAAGTCCAAGGTTGCCAGCTGATTGTCACAGCATCTGATGAG
 ACTCCTGCAACCCAGTCTGAGAGCTATCTTATCCGGCTGCCCTGATGTTGCTTCAGAATGCCACCAACTC
 CCTTACTATGACGTGGGACGCTGCCCTGTTAAGACTTGTGAGGGCAGCAGGATAATGGGATCAGGTGCCGTG
 ATGTCGTGCAAGACTGCTGTGCACTTCAAGACAGAGGAAAGGGAGATCAGTGCAGTGGCTACACGCTACCC
 ACCAAGGTGGCCAAGGGAGTGCAGCTGCCAGCGGTGTACGGAAACTCGGAGCATCGTGCGGGGCCGTGAGTGC
 TGCTGACATGGGGAGCCATGCCCTGGCATGTGACATGGGAACAGCCGTGTAAGCATGACTGGCTACA
 AGGGCACTTTACCCCTCCATGTCACGGGAGACTGAGGGCTGCTGAGGAGCTGCAAGGATGCCACCATATCCACA
 GTGAAACTCTGGTCACTAACATCAGACACAGGGCTGTGGGAGGGAGAAGGTGATTICAATTTGAAAATCAAAG
 GAGGAACAAAAGAGAAGACAGAACCTCTCTGGGCAACCTGGAGATTCTGGAGAGGAGGCTCTTAACTGG
 ATGTTCTGAAAGCAGCGGTGCTTGTAAAGGTGAGGGCTACCGGAGTGAAGGGTCTTGCTAGTGAGCAG
 ATCCAGGGGTTGTGATCTCCGTGATTAACCTGGAGGCTAGAACTGGCTTCTGTCACCCCTAGGGCTGGGG
 CGCCTTGGACAGTGTCACTACAGGCCAACAGGGCTGTGGGAGGGACTGCAAGCAGTGGAGTCTCTCTGATG
 CCTACTCTGCCTATGTTGGCAAGCTGGTGTGGGAGGAAGTGCAGCAGTGGAGTCTCTCTAAATTCAAC
 CCAAATGCAATTGGCGTCCCTCAGCCCTATCTCAACAGCTCAACTACCGTGGACGGACATGAGGATCCACG
 GGTTAAAAGACAGCTTCCAGATTAGCATGGCAAGCCAAGGCCAACTCAGCTGAGGAGAGCAATGGGCCCA
 TCTATGCTTGGAGAACCTCCGGCATGTGAAGAGGCCAACCCAGTGCAGGCCACTTCCGGTTCTACAGGAT
 GAGGGGGATGATGATGACTAACACACAGTCCCTTCAGCAAGAGATGACCTATGAGCTGGACTGAAGACTATCT
 GGCAATGGTGGCCAAGCCGATGGAATTAGGGCCTGCTATATCAAGGTGAAGATTGTGGGCACTGGAAAGTGA
 ATGTCGATGCCAACATGGGGGCACTCATGGGGGCACTGAGTGGGAGGACTGAGTGGGATGCTATGAGG
 AGCACTGGGACAGGGACAGGCCAACATGTCAGCTGGCTGCTGGAGTTCAAGTCAGTGGGATGCTATGAG
 TCAGGACCGTGTGGACCGCACCCCTGGTGAAGGTCACTTGCAGTCACAAACGACACCAGTGAAGTACACCATGCTGGCA
 TGCTGCATGAGTACCTGGTCAACCAACTTGCACCTGCACTGAGTCACAGGCCAGGACCTCGCACGGCAAGGGAGAT
 CCCTGGGACCCACTGGGACAAACTATGCCATCTACACTGTCACTGACCCCTGCTGGGAGGACTGCTGGCC
 CGCGCTGGCCGGTGTGGTGTGGCACTGGGAGGACTGAGTGGGAGGACTGAGTGGGAGTGGCC
 TCACCTTCACACTGTGAGAGGGCAAGTAGGGCCGCCAGGTGCTTCAAGCAGGAGGACTGAGTGGGAGTGGCC
 TCCCCTGCTGCAGGCACTGTCAAGGAAGACTGCCCTCGAGGAGGAGCAGCGAGCGAGCAGGGTGGCCAGCG
 CCAGGGTGGAGTGGTGGCCTCTGAGACATTCTGAGGTTGCTCAACAGGCCCTGATCAACTAAAGTGGTGG
 ATCTCACCCCTCTGCCCCCTCATTTGATGTCAGCAGGCCATTGAGACTGATGCAACAAACTGTGACTTGGTTAA
 TTAAGCACTCTGTTCTGTAATTGCTGTTGTTCTCATGCTTACTACTTGTCCCCATGCTACTGA
 TTGGCAGTGGCCCCACAATGGCACAATAAGCCCTTGTGAAACTGTTCTTAAATGAAACACAAGAAATT
 GGCCACTGGTAAAACCTGCAGCTCAACTGACTTCATTAATGCCATTAAATGCAAATATACTTCCCTCTCT
 TTTGCATGGTTTGCCCCACCTCTGCAATAGTGATAATCTGATGCTGAAGATCAAATAACCAATATAAAGCATAT
 TTCTGGGCTTGCTCCACAGGACATAGGGCAAGCCTGATCATGTCATACATATAAATGGTGGTAAATAAAG
 AAATAAAACACAATACTTTACTTGAAATGTAATAACTTATTATTTCTTGTCAAATTGGAATTCTAGTGC
 ACATTCAAAAGTTAACGTTAACATAGGGTGTCAACTGTTGACATTCCCTTGTCACTGGAAAGAACATCTCTGGT
 ATCCACAAATTACACCAGGTTGCTAACATGTCATTTGCACTTCCCTTGTCACTGGCTTGTCTGCTAGAAAC
 CCAGTGTAGCCCAGGGCAGATGTCATAAAATGCAACTCTGTTGAAAAAA

FIGURE 72

MVGTKAWVFSFLVLEVTSQLGRQTMLTQS VRRVQPGKKNPSI FAKP ADTLESPGEWTWFNI
DYPGGKGDYERLDAIRFYYGDRV CARPLR LEARTTDWTPAGSTGQVVHGS PREGFWCLNREQ
RPGQNCNSNYTVRFLCPPGSLRRDTERI WSPWSPWSKCSAACGQTGVQTRTRICLAEMVSLCS
EASEEGQHCMGQDCTACDLTCPMGQVNADCACMCQDFMLHGAVSLPGGAPASGAIA YLLTK
TPKLLTQTDSDGRFRIPGLCPDGKSILKITKVKF APIVLTMPKTS LKAATIKA EFVRAETPY
MVMNPETKARRAGQSVSLCCKATGKPRPDKYFWYHNDTLLDPSLYKHE SKLVLRKLQQHQAG
EYFCKAQSDAGAVKS KVAQLIVTASDETPCNP VPESYLIRLPHD C FQNATNSFYYDVGRCPV
KTCAGQQDNGIRC RDAVQNCCG ISKTEEREIQC SGYTLPTKVAKECSCQRCTETRSIVRGRV
SAADNGEPMRFGH VYMGN SRVSMTGYKGTFTLHV PQDTERLVLTFVDRLQKFVN TTKVLPFN
KKGS AVFHEIKMLRRKEPI TLEAMETN IIPLGEVVGEDPM AELEIPSRSFYRQNGE PYIGKV
KASVTFLDPRNISTATAAQ TDLNFINDEGDTFPLRTYGMFSVDFRDEV TSEPLNAGKVKVHL
DSTQVKMPEHISTVKLWSLN PDTGLWEEEGDFKFENQRRNKREDRTFLVGNLEIRERRLFNL
DVPESRRCFVKVRAYR SERFLPSEQI QGVVISVINLEPRTGFLSNPRAWGRFD SVITGPNGA
CVPAFCDDQSPDAYSAYV L A SLAGEELQAV ESSPKFNPNAIGVPQPYLNKLN YRRTDHD PR
VKKTAFQISMAKPRPNSAEE SNGPIYAFENLRACEE APPSAAHFRFYQIEGDRYDYNTVPFN
EDDPMSWTEDYLA WWP KPM EFRACYIKVKIVGPLEVNVR SRNMGGTHRRTVGKLYGIRDVRS
TRDRDQP NVSAAC LEFKCS GMLYDQDRVDRTLKVVI PQGSCR RASVN PMLHEYLVNHLPLAV
NN DTSEYTM LAPLDPLGH NYGIYT VTDQDP RTAKEIALGRCFD GTSDGSSRIMKSNVGVALT
FNCVERQVGRQSAFQYLQSTPAQSPAAGTVQGRVPSRRQQRASRGGQRQGGVVASLRFPRVA
QQPLIN

FIGURE 73

CTGCAAGTTGTTAACGCCTAACACACAAGTATGTTAGGCTTCCACCAAAGTCCTCAATATACTGAATACGCAC
 AATATCTTAACCTTCATATTGGTTTGGGATCTGCTTGAGGTCCCCTTCATTTAAAAAAATACAGAG
 ACCTACCTACCGTAGCATAACATACATATGTGTATATATGTAAACTAGACAAAGATCGCAGATCATAAAGC
 AAGCTCTGCTTAGTTCCAAGAAGATTACAAAGAATTAGAG**ATG**TATTGTCAGATCCCTGTCGATTCTAG
 CCCTTGGGTTACGGTAGCCTCACTGATGCAGCCCTACCCCTTGGTTGGGACATTATGATTGTAAGACT
 CAGATTACCGGAAGAAGGGAAAGTTGGGATTACATGGCCTGCCAGCGGAATCCACGGACATGACAAAATA
 TCTGAAAGTAAACTCGATCCTCCGGATATTACCTGTGGAGACCCCTCTGAGACGTTCTGTGCAATGGCAATC
 CCTACATGTGCAATAATGAGTGTGATGCGAGTACCCCTGAGCTGGCACACCCCCCTGAGCTGATGTTGATT
 GAAGGAAGACATCCCTCACATTGGCAGTCTGCCACTTGAAGGAGTATCCAAGCCTCTCAGGTTAACAT
 CACTCTGCTTGGAGCAAAACCATGGAGCTAACAGACAACATAGTTTACCTTGAATCTGGGCGTCCAGACC
 AAATGATCCTGGAGAAGTCTCGATTATGGACGAACATGGCAGCCCTACAGTTTACAGCTTGTGCAATGGCAATC
 GATGCTTTCACATGGATCCTAAATCCGTGAAGGATTATCACAGCATACGGCTTAGAAATCATTGCAACAGA
 AGAGTACTAACAGGGTATAACAAACAAATTCACATTGAAATCAAAGACAGGTTGGCGCTTTTG
 CTGGACCTCGCCTACGCAATATGGCTCCCTACGGACAGCTGGATAACACAAAGAAACTCAGAGATTCTT
 ACAGTCACAGACCTGAGGATAAGGCTGTTAAGACAGCCGTTGGGAAATATTGTAGATGAGCTACACTTGGC
 ACGCTACTTTACGGATCTCAGACATAAAGGTGCGAGGAAGGTGCAAGTGTAAATCTCATGCCACTGTATGTG
 TGATGACAACAGCAAATTGACATGCGAATGTGAGCACAAACACTACAGGTCAGACTGTGGGAAATGCAAGAAG
 AATTATCAGGCCGACCTGGAGTCCAGGCTCTATCTCCCCTACGGCAACTGAAATACCTGTATCCC
 CAGTATTCCAGTATTGGTACGAATGTCTGCGACAACGAGCTCTGCACTGCCAGAACGGAGGGACGTGCCACA
 ACAACGTGCGCTGCCGTGCCCCGGCGCATACACGGGCACTCTGCGAGAACGCTGCCGTGCGAGGAGGCTGGC
 AGCTGCGCTCCGACTCTGGCAGGGCGCCCCCGCACGGCACCCAGCGCTGCTGCTGACCAACGCTGCT
 GGGAACGCCAGCCCCCTGGTAGGTGTCACCTCCAGCCACACGGACGGGCTGTGCCGTGGGAAAGCA
 GACACAACCCAAACATTGCTACTAACATAGGAAACACACACATACAGACACCCCCACTCAGACAGTGTACAA
 CTAAGAAGGCTAACTGAACTAAGCCATATTATCACCCGTGGACAGCACATCCGAGTCAGACTGTTAATT
 TGACTCCAGAGGAGTTGGCAGCTGTTGATATTACTGCAAAATCACATTGCCAGCTGCCAGAACGCTATT
 TTGGAAAGGCTGCGACAGCCCCAAACAGGAAAGACAAAAACAAACAAACCCGACCTAAAACACATTGGC
 TACTCTAGCGTGGTGCCTAGTACGACTCCGCCAGTGTGAGGACCAACAAATAGCATTCTGCTGTCAG
 GTGCATTGTGGCATAAGGAAATCTGTTACAAGCTGCCATATTGGCCTGCTCCGCTCTGTTGACTGTGCA
 CTGTGCTTACTGAAACGTTGCTCTGTAACCCCTGTTGATCTAGCAGCACTGAGTCCAGTGC
 TGTGTAACAGCCCCCTCTAAAGCGCAAGCCAGTCATACCCCTGTTGATCTAGCAGCACTGAGTCCAGTGC
 GCACACACCCACTATACAGAGTGGCTATAGGAAAAAGAAAGTGTATCTATCCTTTGTTGATCTAAATGAAGTT
 ATTTTCTGAACTACTGTAATATGTAGATTGTTGTTGATCTGCAATTGCAATTGTTGTTGTTGACTG
 GTATCTAACTCGAATCAGCAAAGACTGACATTGTTGTTGTTGTTGTTGTTGACTGTGCA
 GATTCTCTGTAAGGGCAACGAACGTGCTGGCATCAAAGAATATCAGTTACATATATAACAGTGTAA
 TTCCACCAAAGGACATTCTAAATGTTCTGTTGCTTAACACTGGAAGATTAAAGAATAAAACTCCTGCA
 TAAACGATTTCAGGAATTGTTGACTGAAAGATGAAAGAACGCCACCAAGCAGTTACACTCA
 TTACTGATTCTGTGTGGACTGAGTACATTGAGCTGACGAAATTAGTTCCCAGGAAGATGGATTGATGTT
 AGCTTGGACAACCTCTGCAAAATATGAGACTATTCCACTTGGAAAAATTACAACAGCAAAAAAAA
 AAAAAAA

FIGURE 74

MYLSRSLSIHALWTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLK
VKLDPPDITCGDPETFCAMGNPYMCNECDASTPELAHPPELMFDFEGRHPSTFWQSATWK
EYPKPLQVNITLSWSKTIELTDNIVTFESGRPDQMILEKSLDYGRTWQPYQYYATDCLDAF
HMDPKSVKDLSQHTVLEIICTEEYSTGYTTNSKIIHFEIKDRFALFAGPRLRNMASLYGQLD
TTKKLRDFFTVDLIRLLRAVGEIFVDELHLARYFYAISDIKVRGRCKCNLHATVCVYDN
SKLTCECEHNTTGPDCGKCKNYQGRPSPGSYLPPIPGBTANTCIPSISIIGTNVCDNELLH
CQNGGTCHNNVRCLCPAAYTGILCEKLREEAGSCGSDSGQGAPPHTPALLLTLGTAS
PLVF

FIGURE 75

CCCACCGCTCCGGGTGACCTGGGCCAGCCCTCCGGCTGGCTAAGATTGCTGAGGAGGC
 CGGGTAGCTGGCAGGCAGCGACTTCCGAAGGCCGCGTCGGCGAGGTGTCCTCATGACTT
 CTCTTGAGACC**ATG**TCCGTGATTTGCCTGCGTGGTACGGTAAGGGATGGACTGCC
 CCTCTCAGCCTCTACTGATTTACACACCCAAGATTTGGAATGGAGGAGACGGCTCA
 AGAGTTAGCCTTGCAGTGGCCCAGTATCCAGGTGAGGTTCTGCAGAAGGTTGTGACTTT
 AGTATAACATTTCTTCTTCGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTCC
 AGCAGCCATGGCCTTCTGCTCCTGGAGACCCCTGTGGTGGAAATTACAGCTCCTATGACA
 CTACCTGCATTGCCCTAGCCTCCAGGCCATACGCTTCTTGAGTTGACAGCATCATTCA
 AAAGTGAAGTGGCATTAACTATGTAAGTCCCTCTCAGATGGAGTGCAGCTGGAAAAAA
 TCAGGAGGAGCTCAAGTTGCAGCCTCCAGCGTTCTCACTCTGGAGGACACAGATGTGGCAA
 ATGGGGTGAATGGTACACACCCGATGCACCTGGAGCCTGCTCCTAATTCCAATGGAA
 CCAGTGACAGCCCTGGGTATCCTCTCCCTCATCTAACATCATGTGTGCTGCCCTGAATCT
 CATTGAGGAGTTCACCTGCAGAACATTACAGGATCCAAGGAGCTGGTCTGCTGGT
 TGGACCAAACCTCG**TGA**GCCAGCCACCCCTGACCCAAATGAGGAGAGCTCTGATTCTCC
 CCAGGGAGCAGTGATGTCAAACTCTGCTGGTGGAAATCTCATCAGCAGGGAGCCTG
 AAAGGGCATGTCAGTGAAATCTGGGAATGGCTGGATTGGAAACATCTGCCATGTGTATTG
 ATGGCAGAGCTGTTGCCACAAGCGCTTTATTTAGGGTAAATTAAACAAATCCATTCTAT
 TCCTCTGACCCATGCTTAGTACATATGACCTTAACCCCTACATTATGATTCTGGGTT
 GCTTCAGAAGTGTATTTCATGAATCATTGATGATTGATCCCCCAGGATTCTATTG
 TTAATGGCTTCTACTAAAAGCATAAAACTGAGGCTGATTAGTCAGGGCAAAACCAT
 TTACTTACATATTGCTTCAAACTTGCTGTTCATGTTACACAAGCTCTACGGTTTC
 TTGTAACAATAAAATTTGAGTAAATAATGGGTACATTAAACAAACTCAGTAGTACAACC
 TAAACTGTATAAAAGTGTGTAAAATGTATAGCCATTATCCTATGTATAAATTAAATG
 AGGTGGCTTCAGAAATGGCAGAATAAAACTAAAGTGTATTAAAAA
 AAAAG

FIGURE 76

MSVIFFACVVVRDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFSIHF
SSFGDVACMAICSCQCPCPAAFCFLETLWWFTASYDTTCIGLASRPYAFLEFDSDIIQKVKW
HFNYVSSSQMECSLEKIQEELKLQPPAVLTLEDVANGVMNGHTPMHLEPAPNFRMEPVTA
LGILSLILNIMCAALNLIRGVHLAEHSLQDPRSWFCWLQTS

77/330

FIGURE 77

TGCTTCCTGGAGACCCTGTGGTGGATTACAGCTCNTATGACACTACCTGCATTGGCNT
AGCCTCCAGGCCATACGCTTTCTTGAGTTGACAGCATCATTCAAAAGTGAAGTGGCATT
TTAACTATGTAAGTTCCNTCAGATGGAGTGCAGCTGGAAAAAATTCAAGGAGGAGCTCAAG
TTGCAGCCTCCAGCGTTCTCANTATGGAGGACACAGATGTGGCAAATGGGT

FIGURE 78

CTCAGCGGCCTCCTCGTAGCGAGCCTAGTGGCGGGTGTGCATTGAAACGTGAGCGCGA
 CCCGACCTTAAAGAGTGGGGAGCAAAGGGAGGACAGAGCCCTTAAAACGAGGCGGGTGGT
 CCTGCCCTTAAGGGCGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCGAGTT
 TCTGTGCAGGCTCGAGGAAAGGCCCCTAGGCTGGTCTGGGTGCTTGGCGGGCGGCTT
 CCTCCCCGCTCGTCCCTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTA
TGGAAGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGC
 GAGTGTATTATATCAACACTTCTGTTGCAACACTGTACATCCTCTGCCACATCTCCTGAC
 CCGCTTCAAGAACGCTGCTGAGTTACCACAGTGGATGATGAAGATGCCACCGTCAACAAGA
 TTGCGCTCGAGCTGTGCACCTTACCCCTGGCAATTGCCCTGGTGTCTGCTCTGCC
 TTCTCCATCATCAGCAATGAGGTGCTGCTCCCTGCCCTCGGAACACTACATCCAGTGGCT
 CAACGGCTCCCTCATCCATGGCCTCTGGAACCTGTTTCTCTTCCCAACCTGCTCCCTCA
 TCTTCCTCATGCCCTTGCAATTCTCACTGAGTCTGAGGGCTTGCTGGCTCCAGAAAG
 GGTGTCTGGGCCGGTCTATGAGACAGTGGTGTGATGCTCCTCACTCTGCTGGTGCT
 AGGTATGGTGTGGGTGGCATCAGCATTGTGGACAAGAACAAAGGCCAACAGAGAGTCAC
 ATGACTTTGGGAGTACTATCTCCCTACCTCTACTCATGCATCTCCTTGGGTTCTG
 CTGCTCTGGTGTACTCCACTGGGTCTGCCCGCATGTTCTCCGTCACTGGGAAGCTGCT
 AGTCAAGCCCCGGCTGCTGGAAGACCTGGAGGAGCAGCTGTACTGCTCAGCCTTGAGGAGG
 CAGCCCTGACCCGCAGGATCTGTAATCCTACTTCTGCTGGCTGCCCTAGACATGGAGCTG
 CTACACAGACAGGTCTGGCTCTGCAGACACAGAGGGCCTGCTGGAGAAGAGGCCAACGG
 TTCAGCCTGGCAACGGAACCTGGCTACCCCTGGCTATGCTGTGCTTGGTGTGACGG
 GCCTGTCATGCTCATTGTGGCCATCCACATCCTGGAGCTGCTCATCGATGAGGCTGCCATG
 CCCCAGGGCATGCAGGGTACCTCCTAGGCCAGGTCTCCTCTCCAAGCTGGCTCCTTGG
 TGCCGTCAATTGAGGTTGACTCATCTTACCTAATGGTGTCTCAGTTGTGGCTTCTATA
 GCTCTCCACTCTCCGGAGCCTGCCAGATGGCACAGACACTGCCATGACGCAGATAATT
 GGGAACTGTGTCTGCTCCTGGCTTAAGCTCAGCACCTCTGCTCTCTCGAACCCCTGG
 GCTCACTCGCTTGACCTGCTGGGTGACTTGGACGCTCACTGGCTGGCAATTCTACA
 TTGTGTTCTCTACAACGCAGCCTTGCAGGCCTCACCACACTCTGCTGGTGAAGACCTTC
 ACTGCAGCTGTGCGGGCAGAGCTGATCCGGGCTTGGACAGACACTGCCGCTGCCGT
 CTCCGGTTCCCCCAGGCATCTAGGAAGACCCAGCACCAG**TGAC**CTCCAGCTGGGGTGGGA
 AGGAAAAAAACTGGACACTGCCATCTGCTGCCAGGCCCTGGAGGGAAGCCAAGGCTACTTGG
 ACCTCAGGACCTGGAATCTGAGAGGGTGGTGGCAGAGGGAGCAGAGCCATCTGCACTATT
 GCATAATCTGAGCCAGAGTTGGGACCGAGCACCTCCTGCTTCCATACCTAACTGTGGCCT
 CAGCATGGGTAGGGCTGGGTGACTGGGTCTAGCCCTGATCCAAATCTGTTACACATCA
 ATCTGCCCTCACTGCTGTTGGCCATCCCCATGCCATGTTACATGATTGATGTGCAAT
 AGGGTGGGTAGGGCAGGGAAAGGACTGGGCCAGGGCAGGCTGGAGGAGATAGATTGTCTCC
 CTTGCCTCTGGCCAGCAGGCCTAAGCACTGTGCTATCCTGGAGGGCTTGGACCACCTG
 AAAGACCAAGGGATAGGGAGGAGGAGGCTTCAGCCATCAGCAATAAGTTGATCCCAGGG
 AAAAAA

FIGURE 79

MEAPDYEVLSVREQLFHERIRECIISTLLFATLYILCHIFLTRFKPAEFTTVDDEDATVNK
IALELCFTLAIALGAVLLLPSIISNEVLLSLPRNYYIQWLNGSLIHGLWNLVFLFPNLSL
IFLMPFAYFFTESEGAGSRKGVLGRVYETVVMLMLTLLVLGMVWVASAIVDKNKANRESL
YDFWEYYLPYLYSCISFLGVLLLLVCTPLGLARMFSVTGKLLVKPRLLEDLEEQLYCSAFEE
AALTRRICNPTSCWLPLDMELLHRQVLALQTQRVLLEKRRKASAWQRNLGYPLAMLCLLVLT
GLSVLIVAIHILELLIDEAAMPRGMQGTSLGQVSFSKLGSFGAVIQVVLIFYLMVSSVGFY
SSPLFRSLRPRWHTAMTQIIGNCVCLVLSSALPVFSRTLGLTRFDLLGDFGRFNWLGNFY
IVFLYNAAFAGLTTLCLVKTFTAVERAELIRAFGLDRLPLPVSGFPQASRKTQHQ

FIGURE 80

GGCTGCCGAGGGAAAGGCCCTGGGTTGGTCTGGTGGCTTGGCGGCAGNTCC
GCTCGTCCTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGAAGC
ACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGTGT
TTATATCAACACTTCTGTTGCAACACTGTACATCCTCTGCCACATCTTCCTGACCCGCTTC
AAGAAGCCTGCTGAGTTACCACAGTGGATGATGAAGATGCCACCG

FIGURE 81

GACCGACCTTAAAGAGTGGGAGCAAAGGGAGGCAGAGCCTTTAAAACGAGGCGGTGGTGC
CTGCCCTTAAGGGCGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCGAGTTTC
TGTGCGAGGCTGCGAGGAAAGGCCCTAGGCTGGTCTGGTGCCTGGCGGCGGCTTCCT
CCCCGTTGTCNTCCCCGGGCCAGAGGCACCTCGGCTCAGTCATGCTGAGCAGAGTATGGA
AGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGT
GTATTATATCAACACTTCTGTTGCAACACTGTACATCNTCTGCCACATCTCCTGACCCGC
TTCAAGAAGCCTGCTGAGTTACCAAGTGGATGATGAAGATGCCACCGTCAACAAGATTGC
GCTCGAGCTGTGCACCTTACCCCTGGCAATTGCCCTGGTGCTGTCCTGCTGCCCTTCT
CCATCATCAGCAATGAGGTGCTGCACTCCC

FIGURE 82

GATGTGCTCCTGGAGCTGGTGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTTT
GGAATTGAGGAAACTTCTCTTTGATCTCAGCCCTGGTGGTCCAGGTCTTC**ATG**CTGCTGT
GGGTGATATTACTGGTCCTGGCTCCTGTCAGTGGACAGTTGCAAGGACACCCAGGCCATT
ATTTCCAGCCTCCATGGACCACAGTCTCCAAGGAGAGAGTGACCCCTACTTGCAA
GGGATTCGCTTCACTCACCAACAGAAAACAAATGGTACCATCGGTACCTGGAAAGAAA
TACTAAGAGAAACCCAGACAATATCCTGAGGTTAGGAATCTGGAGAGTACAGATGCCAG
GCCAGGGCTCCCTCTCAGTAGCCCTGTGCACTTGGATTTCTTCAGAGATGGGATTCC
TCATGCTGCCAGGCTAACAGCTCGCTGATCCTGCAAGCTCCACTTCTGTGTTGAAGGAGAC
AAAGCGCTGGATTACAGCTCGCTGATCCTGCAAGCTCCACTTCTGTGTTGAAGGAGAC
TCTGTGGTTCTGAGGTGCCGGCAAAGGCGGAAGTAACACTGAATAATACTATTACAAGAA
TGATAATGTCCTGGCATTCTTAATAAAAGAACTGACTTCCAAAAAAA
AAA

FIGURE 83

MLLWVILLVLAPVSGQFARTPRPIIFLQPPWTTVFQGERVLTCKGFRFYSPQTKWYHRYL
GKEILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFSSEMGPAAQANVELLGSSDLT

FIGURE 84

CAGAAGAGGGGCTAGCTAGCTGTCTCGGGACCAGGGAGACCCCCCGC GCCCCCCCGGTGT
 GAGGCGCCCTCACAGGGCCGGTGGCTGGCGAGCCGACGCCGGCGGAGGAGGCTGTGAG
 GAGTGTGTGGAACAGGACCCGGGACAGAGGAACC**ATGG**CTCCGCAGAACCTGAGCACCTTT
 GCCTGTTGCTGCTATACTCATCGGGCGGTGATTGCCGGACGAGATTCTATAAGATCTTG
 GGGGTGCCCTCGAAGTGCCTCTATAAAAGGATATTAAAAAGGCCTATAGGAAACTAGCCCTGCA
 GCTTCATCCCACCGGAACCCCTGATGATCCACAAGCCCAGGAGAAATTCCAGGATCTGGGTG
 CTGCTTATGAGGTTCTGTCAGATAGTGAGAACGGAAACAGTACGATACTTATGGTGAAGAA
 GGATTAAAAGATGGTCATCAGAGCTCCATGGAGACATTTTCACACTTCTTGAGGATT
 TGGTTTCATGTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATTCCAAGAGGAAGTGATA
 TTATTGTAGATCTAGAAGTCACTTGGAAAGAAGTATATGCAGGAAATTGTGAAGTAGTT
 AGAAACAAACCTGTGGCAAGGCAGGCTCCTGGCAAACGGAAGTGCAATTGTCGGCAAGAGAT
 GCGGACCAACCAGCTGGGCCCTGGCGCTTCAAATGACCCAGGAGGTGGTCTGCGACGAAT
 GCCCTAATGTCAAACACTGTGAATGAAGAACGAACGCTGGAAGTAGAAATAGAGCCTGGGTG
 AGAGACGGCATGGAGTACCCATTATTGGAGAAGGTGAGCCTCACGTGGATGGGAGCCTGG
 AGATTACGGTCCGAATCAAAGTTGTCAAGCACCCATATTGAAAGGAGAGGAGATGATT
 TGTACACAAATGTGACAATCTCATTAGTTGAGTCACTGGTTGGCTTGAGATGGATATTACT
 CACTTGGATGGTCACAAGGTACATATTCCCGGGATAAGATCACCAAGGCCAGGAGCGAAGCT
 ATGGAAGAAAGGGGAAGGGCTCCCAACTTGACAACAACAATATCAAGGGCTTTGATAA
 TCACCTTGATGTGGATTTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAA
 CAGCTACTGAAACAAGGGTCAGTGCAGAACGGTATAACATGGACTGCAAGGATAT**TGA**GAGTG
 AATAAAATTGGACTTGTAAATAAGTGAATAAGCGATATTATTCTGCAAGGTTTT
 TTGTGTGTGTTTTGTTTATTTCATATGCAAGTTAGGCTTAATTGTTATCTAATGA
 TCATCATGAAATGAATAAGAGGGCTTAAGAATTGTCCATTGCATTGGAAAAGAATGACC
 AGCAAAAGGTTACTAACACCTCTCCCTTGGGATTAAATGCTGGTGTGCCGCCCTGAGT
 TTCAAGAATTAAAGCTGCAAGAGGACTCCAGGAGCAAAAGAAACACAATATAGAGGGTTGGA
 GTTGTAGCAATTCAAAATGCCAACTGGAGAAGTCTGTTTAAATACATTGTT
 TTATTTTA

FIGURE 85

MAPQNLSTFCLLLYLIGAVIAGRDFYKILGVPRSASIKDIKKAYRKLAQLHPDRNPDDPQ
AQEKFQDLGAAYEVLSDEKRKQYDTYGEEGLKDGHQSSHGDIFSHFFGDFGMFGGTPRQQ
DRNIPRGSDIIVDLEVYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQ
MTQEVCVCDECPNVKLVNEERTLEVEIEPGVRDGMEYPFIGECEPHVDGEPGDLRFRIKVVKH
PIFERRGDDLYTNVTISLVESLGFEMDITHLDGHKVHISRDKITRPGAKLWKGEGLPNFD
NNNIKGSLIITFDVDFPKEQLTEEARREGIKQLLQGSVQKVYNGLQGY

Important features:

Signal peptide:

amino acids 1-22

Cell attachment sequence.

amino acids 254-257

Nt-dnaJ domain signature.

amino acids 67-87

Homologous region to Nt-dnaJ domain proteins.

amino acids 26-58

N-glycosylation site.

amino acids 5-9, 261-265

Tyrosine kinase phosphorylation site.

amino acids 253-260

N-myristoylation site.

amino acids 18-24, 31-37, 93-99, 215-221

Amidation site.

amino acids 164-168

FIGURE 86

TGGGACCAGGAACCCGGCCCCCGGTGGAGNGCTAACAGGCCGGTGGNTGCGACCGAA
GC GG C GGG CGG AGG AGG TTT GAGG AT TTT GGA ACAGG ACC CGG ACAG AGGA ACCAT GG TT
CCG CAGA ACNT GAGC ACNTT GCCT GTT GNT AT ACTTC AT CGGG CGGT GATT GCC CG
ACG AGA ATT NTATAAG AT T TGGGT GCCT NGA AGT GCCT NTATAA AGG AT ATT AAAA AGG
CCT ATAGGAA ACTAG CCCT GCAG NT ATCCG ACC CGGA ACC CTG ATG ATCC ACA AGCC CAG
GAG AA ATT CCAGG AT TGGGT GCT GCT TAT GAGG TT NT GTC AGA TAGT GAG AA AC GG AA ACA
GTAC GATA ATT ATGGT GAAG AAGG AT AAAG ATGGT NATC AGAG CTCC ATGG AGAC AT TT
TTTCACACTNTTGGGATTTGGTTCATGTTGGAGGAACCCCTNGTCAGCAAGACAGA
AATATTCCAAGAG

FIGURE 87

GGCACGAGGC GGCGGGG CAGTC GCGGGAT GCGCC CGGAGCC ACAGC CTGAGGCC CT CAGGT
CTCTGCAGGTGTCGTGGAGGAACCTAGCACCTGCCATCCTCTTCCCCAATTGCCACTTCCA
GCAGCTTAGCCC ATGAGGAGGAT GTGACCGGGACTGAGTCAGGAGCCCTCTGGAAAGC**ATGG**
AGACTGTGGTGATTGTTGCCATAGGTGTGCTGGCCACC ATCTTCTGGCTTCGTTGCAGCC
TTGGTGCTGGTTGCAGGCAGCGCTACTGCCGGCCGCGAGACCTGCTGCAGCGCTATGATT
TAAGCCCATTGTGGACCTCATTGGTGC CATGGAGACCCAGTCTGAGCCCTCTGAGTTAGAAC
TGGACGATGTCGTTATCACCAACCCCCACATTGAGGCCATTCTGGAGAATGAAGACTGGATC
GAAGATGCCTCGGGTCTCATGTCCC ACTGC ATTGCCATCTGAAGATTGTCACACTCTGAC
AGAGAAGCTTGTGCCATGACAATGGGCTCTGGGGCAAGATGAAGACTTCAGCCAGTGTCA
GCGACATCATTGTGGTGGCCAAGCGGATCAGCCCCAGGGTGGATGATGTTGTGAAGTCGATG
TACCCCTCCGTTGGACCCCAA ACTCCTGGACGCACGGACGACTGCCCTGCTCCTGTCTGTCAG
TCACCTGGTGCTGGTGACAAGGAATGCCTGCCATCTGACGGAGGCCTGGACTGGATTGACC
AGTCTCTGTCGGCTGCTGAGGAGCATTGGAAGTCCTCGAGAAGCAGCCCTAGCTCTGAG
CCAGATAAAGGCCCTCCAGGCCCTGAAGGCTCCTGCAGGAGCAGTCTGCAATT**TAG**TGCCT
ACAGGCCAGCAGCTAGCCATGAAGGCCCTGCCGCCATCCCTGGATGGCTCAGCTTAGCCTT
CTACTTTCTATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTTGAGCTGTGTGCATAG
TAAAGCAGGAGATCCCCGT CAGTTATGCCTCTTGCAGTTGCAA ACTGTGGCTGGT GAGT
GGCAGTCTAATACTACAGTTAGGGAGATGCCATTCACTCTGCAAGAGGGAGTATTGAAAAA
CTGGTGGACTGTCAGCTTATTTAGCTCACCTAGTGTGTTCAAGAAAATTGAGCCACCGTCT
AAGAAATCAAGAGGTTCACATTAAAATTAGAATTCTGGCCTCTCGATCGGT CAGAATG
TGTGGCAATTCTGATCTGCATTT CAGAAGAGGACAATCAATTGAAACTAAGTAGGGGTTTC
TTCTTTGGCAAGACTTGTACTCTC ACCTGGCCTGTTCAATTATTGTATTATCTGCCT
GGTCCCTGAGGCGTCTGGCTCTCCTCTCCCTTGCAAGGTTGGGTTGAAGCTGAGGAAC
ACAAAGTTGATGATTCTTTATCTTATGCCTGCAATTACCTAGCTACCACTAGGTG
GATAGTAAATTATACTTATGTTCCCTCAAAAAAAAAAAAAAA

FIGURE 88

METVVIVAVGVLATIFLASFAALVLVCRQRYCRPRDLLQRYDSKPIVDLIGAMETQSEPSEL
ELDDVVITNPHEIAILENEDWIEDASGLMSHCIAILKICHTLEKLVAMTMGSGAKMKTSA
VSDIIVVAKRISPRVDDVVKS MYPPLDPKLLDARTTALLLSVSHLVLVTRNACHLTGGLDWI
DQSLSAEEHLEVLR EAA LASEPDKG LPGPEGFLQE QSAI

FIGURE 89

GCTTCATTCCTCCGACTCAGCTCCCACCCCTGGGCTTCCGAGGTGCTTCGCCGCTGTCC
CCACCACTGCAGCCATGATCTCCTAACGGACACGCAGAAAATTGGAATGGGATTAACAGGA
TTGGAGTGTTCCTGTCTTGAAATGATTCTCTTTGACAAAGCACTACTGGCTAT
TGGAAATGTTTATTGTAGCCGGCTTGGCTTGTAATTGGTTAGAAAGAACATTAGAT
TCTTCTTCCAAAAACATAAAATGAAAGCTACAGGTTTTCTGGGTGGTGTATTGTAGTC
CTTATTGGTTGGCCTTGATAGGCATGATCTCGAAATTATGGATTTCTCTGTTCAAG
GGGCTTCTTCCTGCGTTGGCTTATTAGAAGAGTGCCAGTCCTGGATCCCTCCTAAAT
TTACCTGGAATTAGATCATTTGTAGATAAAGTTGGAGAAAGCAACAATATGGTATAACAACA
AGTGAATTGAAGACTCATTAAATATTGTGTTATTATAAAGTCATTGAAGAATATTCA
GCACAAAATTAAATTACATGAAATAGCTGTAAATGTTCTTACAGGAGTTAAACGTATAG
CCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGTGAAACAGGCTCTACTCAAGTGA
ACTAAGAAGAAGTCAGCAAGCAAACGTGAGAGAGGTGAAATCCATGTTAATGATGCTTAAGAA
ACTCTTGAAGGCTATTGTGTTGTTCCACAATGTGCGAAACTCAGGCATCCTTAGAGAA
CTGTGGTGCCTGTTCTTTCTTTATTGAAAGGCTCAGGAGCATCCATAGGCATTGCT
TTTAGAAGTGTCCACTGCAATGGAAAAATATTCCAGTTGCACTGTATCTGGAAAGTGA
TGCATGAATTGATTGGATTGTGTCAATTAAAGTATTAAACCAAGGAAACCCAATTG
ATGTATGGATTACTTTTTTGNGNCNCAGGGCC

FIGURE 90

MISLTDTQKIGMGLTGFVFFLFFGMILFFDKALLAIGNVLFVAGLA
FVIGLERTFRFFFQK
HKMKATGFFLGGVFVVLIGWPLIGMIFEIYGFLLFRGFPVVVGFI
RRVPVLGSLLNLPGI
RSFVDKVGESNNMV

Important features:

Transmembrane domains:

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

N-myristoylation sites.

amino acids 11-16, 51-56 and 116-121

Aminoacyl-transfer RNA synthetases class-II protein.

amino acids 49-59

FIGURE 91

GAAGACGTGGCGCTCTGCCTGGCTGTTCCCGCTTCATTCTCCGACTCAGCTTCCC
ACCNTGGGCTTCCGAGGTGCTTCGCCGCTGTCCCCACCACTGCAGCCATGATCCTTAA
CGGACACGCAGAAAATTGGAATGGGATTAACCGGATTGGAGTGTTTCCCTGTTGGGA
ATGATTCTCTTTGACAAAGCACTACTGGCTATTGAAATGTTTATTGTAGCCGGCTT
GGCTTTGTAATTGGTTAGAAAGAACATTCAATTCTTCTTCAAAAACATAAAATGAAAG
CTACAGGTTTTCTGGGTGGTGTATTGTAGTCCTTATTGGTTGGCCTTGATAGGCATG
ATCTCGAAATTATGGATTTCTCTTGTTC

FIGURE 92

GGCACGAGGCTGAACCCAGCCGGCTCCATCTCAGCTCTGGTTCTAAGTCATGTGCCAA
 GGCTGCCAGGAAGGAGACGCCCTCCTGAGTCCTGGATCTTCTCCTCTGGAAATCTTGA
 CTGTGGTAGTTATTCTGAATAAGAGCGTCCACGCATC**ATG**GACCTCGCGGGACTGC
 TGAAGTCTCAGTCCTGTGCCACCTGGTCTTGCTACGTCTTATTGCCTCAGGGCTAATC
 ATCAACACCATTCACTCAGCTCTCCTCCTCTGGCCCATTAAACAAGCAGCTCTCCGGAA
 GATCAACTGCAGACTGTCTATTGCATCTCAAGCCAGCTGGTGATGCTGCTGGAGTGGTGGT
 CGGGCACGGAATGCACCATCTCACGGACCCCGCGCCTACCTCAAGTATGGGAAGGAAAAT
 GCCATCGTGGTCTCAACCACAAGTTGAAATTGACTTCTGTGTGGCTGGAGCCTGTCCGA
 ACGCTTGGGCTGTTAGGGGCTCCAAGGTCTGGCCAAGAAAGAGCTGCCATATGTCCCAA
 TTATCGGCTGGATGTGGTACTTCACCGAGATGGTCTTCTGTTCGCGCAAGTGGGAGCAGGAT
 CGCAAGACGGTTGCCACCAGTTGCAGCACCTCCGGACTACCCCGAGAAGTATTTTCCT
 GATTCACTGTGAGGGCACACGGTACCGAGAAGAACATGAGATCAGCATGCAGGTGGCCC
 GGGCCAAGGGCTGCCCTCGCCTCAAGCATCACCTGTTGCCACGAACCAAGGGCTCGCCATC
 ACCGTGAGGAGCTTGAGAAATGTAGTTCAGCTGTATATGACTGTACACTCAATTTCAGAAA
 TAATGAAAATCCAACACTGCTGGGACTCTAAACGGAAAGAAATACCATGAGATTGTATG
 TTAGGAGGATCCACTGGAAGACATCCCTGAAGACGATGACGAGTGCTGGCCTGGCTGCAC
 AAGCTTACCACTCAGGAGAAGGATGCCTTCAGGAGGAGTACTACAGGACGGGCACCTCCCAGA
 GACGCCATGGTCCCCCGGCCCTGGACCCCTCGTAACGGCTGTTGGCTGTTGGCCTCGC
 TGGTGCCTACCCCTTCTTCAGTTCTGGTCAAGCATGATCAGGAGCGGGCTTCCCTGACG
 CTGGCCAGCTTCATCCTCGTCTTGTGGCTCCGTGGAGTTGATGGATGATTGGTGT
 GACGGAAATTGACAAGGGCTCTGCCCTACGGCAACTCTGACAGCAAGCAGAAACTGAATGACT
GACTCAGGGAGGTGTCACCATCCGAAGGGAACCTGGGAACGGTGGCCTCTGCATATCCT
 CCTTAGTGGGACACGGTGACAAAGGCTGGGTGAGCCCTGCTGGCACGGCGGAAGTCACGA
 CCTCTCCAGCCAGGGAGTCTGGTCTCAAGGCCGGATGGGGAGGAAGATGTTTGTAAATCTT
 TTTTCCCCATGTGCTTAGTGGCTTGGTTCTTGTGCGAGTGTGTGAGAATGGC
 TGTGTGGTGAGTGTGAACTTGTGATCATAGAAAGGGTATTTAGGCTGCAGGGAG
 GGCAGGGCTGGGACCGAAGGGACAAGTCCCCTTCATCCTTGGTGTGAGTTCTGT
 AACCCCTGGTTGCCAGAGATAAGTGAAAAGTGTCTTAGGTGAGATGACTAAATTATGCCTC
 CAAGAAAAAAAAATTAAAGTGTCTTCTGGTCAAAAAAA

FIGURE 93

M D I A G L L K S Q F L C H L V F C Y V F I A S G L I I N T I Q L F T L L W P I N K Q L F R K I N C R L S Y C I S S Q L V
M L L E W W S G T E C T I F T D P R A Y L K Y G K E N A I V V L N H K F E I D F L C G W S L S E R F G L L G G S K V L A K K
E L A Y V P I I G W M W Y F T E M V F C S R K W E Q D R K T V A T S L Q H L R D Y P E K Y F F L I H C E G T R F T E K K H E
I S M Q V A R A K G L P R L K H H L P R T K G F A I T V R S L R N V V S A V Y D C T L N F R N N E N P T L L G V L N G K K
Y H A D L Y V R R I P L E D I P E D D D E C S A W L H K L Y Q E K D A F Q E E Y Y R T G T F P E T P M V P P R R P W T L V N
W L F W A S L V L Y P F F Q F L V S M I R S G S S L T L A S F I L V F F V A S V G V R W M I G V T E I D K G S A Y G N S D S
K Q K L N D

FIGURE 94

CTGAGGC GGCGGTAGC **ATG** GAGGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTGCTCG
 GCGCACTCGCTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTCTTCTGGGAA
 GTAAAAGGTGAAGCCAAGAACAGCATTACTGATTCCCAAATGGATGATGTTGAAGTTGTTA
 TACAATTGACATTCAAGAAATATATTCCATGCTATCAGCTTTAGCTTTATAATTCTTCAG
 GCAGAAGTAAATGAGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGT
 TGGTACAAATTCCCGTCGTCAATTCAAGATCATGACGTTAGAGAGAGGCTGCTTCACAA
 AAACTTGCAGGAGCATTTCAAACCAAGACCTGTTCTGCTATTACACCAAGTATAA
 TAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCTTATATAAACCTCAAAAAGGACTT
 TTTCACAGGGTACCTTAGTGGTTGCCAATCTGGGATGTCTGAACAACACTGGGTTATAAAAC
 TGTATCAGGTTCTGTATGTCCACTGGTTAGCCGAGCAGTACAAACACACAGCTCTAAAT
 TTTTGAAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAATGAAATGTATGCTTCATTA
 CAAGAGGAATTAAAGAGTATATGCAAAAAAGTGGAAAGACAGTGAACAAGCAGTAGATAAAACT
 AGTAAAGGATGTAACACAGATTAAACGAGAAATTGAGAAAAGGAGAGGAGCACAGATTCAAG
 CAGCAAGAGAGAAGAACATCCAAAAGACCCTCAGGAGAACATTTCCTTGTCAAGGCATTA
 CGGACCTTTTCCAAATTCTGAATTCTCATTCACTGTGTTAGTGTCTTAAAAAATAGACA
 TGTTCTAAAGTAGCTGTAACTACAACCACCATCTCGATGTAGACAATCTGACCTTAA
 TGGTAGAACACACTGACATTCCCTGAAGCTAGTCCAGCTAGTACACCACAAATCATTAAGCAT
 AAAGCCTTAGACTAGATGACAGATGGCAATTCAAGAGATCTGGTTTAGATACACAAGA
 CAAACGATCTAAAGCAAATCTGGTAGTAGTAACCAAGATAAAGCATCCAAAATGAGCAGCC
 CAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTGGTGAATATTACGGTCTCCTACA
 TTT**TGA**TCCTTTAACCTTACAAGGAGATTTTTATTGGCTGATGGTAAAGCCAAACAT
 TTCTATTGTTTACTATGTTGAGCTACTTGCAGTAAGTCATTGTTACTATGTTCAC
 CTGTTGCAGTAATACACAGATAACTCTTAGTGCATTACTCACAAAGTACTTTCAAAC
 ATCAGATGCTTTATTCCAAACCTTTTCACCTTCACTAAGTGTGAGGGGAAGGCT
 TACACAGACACATTCTTACAATTGAAAAGTGAAGGACAGGACAGTGGCTCACACCTGAA
 TCCCAGCACTAGGAAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCC
 TGGGCAACGTATTGAGACCATGTCTATTAAAAAATGGAAAAGCAAGAATAGCCTTAT
 TTTCAAAATATGAAAGAAATTATGAAAATTCTGAGTCATTAAATTCTCCTTAAG
 TGATACTTTTAAAGTACATTATGGCTAGAGTGTGCCAGATAAAATGCTGGATATCATGCA
 ATAAATTGCAAAACATCATCTAAAATTAAAAAAAAAAAAAAAAAAAAAA

FIGURE 95

MEGESTSAVLSGFVLGALAFQHLNTSDTEGFLLGEVKGEAKNSITDSQMDDVEVVYTIDIQ
KYIPCYQLFSFYNSSGEVNEQALKKILSNVKNVVGWYKFRRHSDQIMTFRERLLHKNLQEHE
FSNQDLVFLLLTPSIITESCSTHRLEHSLYKPQKGLFHRVPLVANLGMSEQLGYKTVSGSC
MSTGFSRAVQTHSSKFFED GSLKEVHKINEMYASLQEELKSICKVEDSEQAVDKLVKDVN
RLKREIEKRRGAQIQAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVS KSS
CNYNHLDVVDNLTL MVEHTDIPEASPASTPQIIKHKA LD LDDR WQFKRSRLLDTQDKRSKA
NTGSSNQDKASKMSSPETDEEIEKMKGFG EYSRSPTF

FIGURE 96

GGCACAGCCGCGCGGGAGGGCAGAGTCAGCCGAGCGAGTCCAGCCGGACGAGCGGACCAGCGCAGGGCAGC
 CCAAGCAGCGCGCAGCGAACGCCGCCGCCACACCCCTCTGGGTCCCCGGCGCTGCCACCCCTCCCT
 CCTTCCCCCGCTCCCCGCCCTGCCGGCCAGTCAGCTTGCGGGTCTCGCTGCCCGCAAACCCGAGGTACCCA
 GCCCGCGCCTCTGCTCCCTGGCCGCCGCCCTCACGCCCTCCTCTCCCTGGCCGGCGCTGGCACC
 GGGGACCGTTGCCTGACGCGAGGCCAGCTACTTTGCCCGCTCTCCCTGCCCTGCTGCCCTTCCAC
 CAACTCCAACCTCTTCTCCCTCAGCTCCACTCGTAGTCCCAGCTCCGCCAGCCCTGCCGCTGCCGTAG
 CGCGCTTCCCGTCCGGTCCAAAGGTGGAAACGCGTCCGCCGCCGCCACCATGGCACGGTTGGCTTGC
 CGCGCTTCTGCACCCGGCAGTGTCAAGCAGCTCAAGTCAGAAGTTGCTCG
 AAGTGCAGCTTACGTGTCACAGATGAGATGCCCTCCACGAGATCAACGGTATCAT
 TTGAAGATCTGCCCCAGGGTTCTACCTGCTCTCAAGAGATGGAGGAGAAGTACAGCCTGCAAAGTAAAGA
 TGATTTCAAAAGTGTGGTCAGCGAACAGTCAATCATTTGAAAGCTTGTGAAAGACATATGGCCAT
 ATGAATTCTTCAAAGAACTACTGAAAATCAGAGAAATCCCTGAATGATAATGTTGTGAAGACATATGGCCAT
 TTATACATGCAAATCTGAGCTATTAAAGATCTCTCGTAGAGATTGAAAGCTTACTACGTGGTGGAAATGT
 GAACCTGGAAGAAATGCTAAATGACTTCTGGCTCGCCTCTGGAGCGGATGTTCCGCTGGTGAACCTCCAGT
 ACCACTTACAGATGAGTACTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAGGCCCTCGGAGATGTCCCT
 CGCAAATTGAAGCTCCAGGTTACTCGTGCTTTGAGCAGCCGTAAGGCTTAGCGTTGCGGG
 AGATGTCGTGAGCAAGGTCTCCGTGTAACCCCCACAGCCCAGTGTACCCATGCCCTGTGAAGATGATCTACT
 GCTCCCACGCCGGGTCTCGTAGCTGAAAGCCATGTTACAACACTGCTCAAACATCATGAGAGGCTGTTG
 GCCAACCAAGGGGATCTGATTTGAATGAAACAATTTCATAGATGCTATGCTGATGGTGGCAGAGAGGCTAGA
 GGGTCTTCAACATTGAATCGGTATGGATCCCCTCGATGTGAAGATTCTGATGCTATTATGAACATGCAGG
 ATAATAGTGTCAAGTGTCTCAGAAGGTTCCAGGGATGTGGACCCCCAACGCCCTCCAGCTGGACGAATT
 TCTCGTTCCATCTGAAAGTGCCTCAGTGCTCGCTCAGACCACATCACCCGAGGAACGCCAACACAGC
 AGCTGGCACTAGTTGGACCGACTGGTACTGATGTCAGGAGAAACTGAAACAGGCAAGAAATTCTGGTCCT
 CCCTTCCGAGCAACGTTGCAACGATGAGAGGATGGCTGCAGGAAACGGCAATGAGGATGACTGTTGAATGG
 AAAGGCAAAGCAGGTACCTGTTGAGTGAAGGAATGGATTAGCAACCAAGGGCAACAACCCAGAGGTCCA
 GGTTGACACCAGCAAACAGACATACTGATCCTCGTCAAATCATGGCTCTCGAGTGTGACCAAGATGA
 AGAATGCAATGAACTGGGAACGACGTGGACTCTTTGATATCAGTGATGAAAGTAGTGGAGAAGGAAGTGGAAAGT
 GGCTGTGAGTATCAGCAGTGCCCTCAGAGTTGACTACAATGCCACTGACCATGCTGGAGAGTGCACATGA
 GAAAGCCGACAGTGTGGTGTCCGTCTGGGCACAGGCCACCTCCTCACTGTCTCTGCATCTGTTCTGG
 TTATGCAGAGAGACTGGAGATAATTCTCAAACCTGAGAAAAAGTGTTCATCAAAAGTAAAAGGCACCAAGT
 ATCACTTTCTACCATCTAGTGACTTGTCTTTAAATGAATGGACAACAATGTACAGTTTACTATGTGGC
 CACTGGTTAAGAAGTGTGACTTGTCTCATTCAGTTGGAGGAAAGGGACTGTGCATTGAGTTGG
 TCCTGCTCCCCAACATGTTAACGTTGCTAACAGTGAGGTACAGAACTATAGTTAGTTGTGCATTGTGA
 TTTTATCACTCTATTATTTGTTGTATGTTTTCTCATTCGTTGTGGGTTTTTCAACTGTGATCT
 CGCCTGTTCTTACAAGCAAACCAGGGCCCTCTGGCACGTAACATGTACGTATTCTGAAATATTAAATA
 GCTGTACAGAAGCAGGTTATTATCATGTTATCTTATTAAAAGAAAAAGCCAAAAAGC

FIGURE 97

MARFGLPALLCTLAVLSAALLAAELKSKCSEVRRLYVSKGFMKNDAPLHEINGDHLKICPQ
GSTCCSQEMEEKYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSINNDMF
VKTYGHLYMQNSELFKDLFVELKRYYVVGNVNLEEMLNDFWARLLERMFRVLVNSQYHFTDEY
LECVSKYTEQLKPGDVPRKLKLQVTRAFVAARTFAQGLAVAGDVSKVSVNPTAQCTHAL
LKMIYCSHCRLTVKPCNYCSNIMRGCLANQGDLDFEWNNFIDAMLMVAERLEGPFNIES
VMDPIDVKISDAIMNMQDNSVQVSQKVFOQCGPPKPLPAGRISRSISESAFSARFRPHPEE
RPTTAAGTSLDRLVTDVKEKLQAKKFWSLPSNCNDERMAAGNGNEDDCWNGKGKSRYLF
AVTGNGLANQGNNEPVQVDTSKPDILILRQIMALRVMTSKMKNAYNGNDVDFDISDESSGE
GSGSGCEYQQCPSEFDYNATDHAGKSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

FIGURE 98

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCT
GACCTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTCATTATATTCTCAA
GCAACTTACAGCTGCACCGACAGTTGCGATGAAAGTTCTAATCTCTCCCTCCTGTG
TGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGTGCAGAGGCCAC
AGGGACCGAGGCCAGGCTCTAGGAGATGGCTCCAGGAAGGCAGCCAAGAAATGTGAGTGAA
AGATTGGTTCTGAGAGCCCCGAGAAGAAAATTCATGACAGTGTCTGGGCTGCCAAAGAAC
AGTGCCCTGTGATCATTCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCAAGA
AAGCCAAACAAGCATTCCAGAGCCTGCCAGCAATTCTCAAACAATGTCAGCTAAGAAC
TGCTCTGCCTTGTAGGAGCTCTGAGCGCCACTCTTCCAATTAAACATTCTCAGCCAAGAA
GACAGTGAGCACACCTACCAGACACTCTTCTCTCCCACCTCACTCTCCACTGTACCCACC
CCTAAATCATTCCAGTGCTCTCAAAAAGCATGTTTCAAGATCATTGTTGCTCTC
TCTAGTGTCTTCTCTCGTCAGTCTTAGCCTGTGCCCTCCCTACCCAGGCTAGGCTT
AATTACCTGAAAGATTCCAGGAAACTGTAGCTCCTAGCTAGTGTCAATTAAACCTAAATGC
AATCAGGAAAGTAGCAAACAGAAGTCAATAATTTAAATGTCAAAAAAAAAAAAAAAA

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FIGURE 99

MKVLISLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRR
KFMTVSGLPKKQCPCDHFKGNVKKTRHQRHHRKPNKHSRACQQFLKQCQLRSFALPL

FIGURE 100

AATGGCCTGCTTAGTACTCGCCTGACAGTTGTCTGGACTGCTTGTCTTATTCCGTACCT
GCTATGCAGACGACAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCA
AAGCCAGACTCCCCAAATTCTAAGCCTCTGGCACAGAGATCATTGAGAATGCAGTCGA
GTTCATCCTCCGCTCCATGTCCAGGAGCACAGGATTATGGAATTGATGATAATGAAGGAA
AACATTCAAATGACATCCTCAGGACACACCCATGTGGCTCCTGGACAATCCAAGAGCA
GCCAAATCCTGCTTTCCAGTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAAC
TCCCAACGAGTTCTCAGGATTCAAGGCTCTGGCTTCAACCAAACAGAACTCATTGAAACACC
CTGACTGCATTTGCTTTAGAAAGTTAGAATAATGGCGCTTGGGATCACATAGTTG
ATGGAGAGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 101

MAVLVLRLTVVLGLLVLFLTCYADDKPDKPDDSGKDPKPDFPKFLSLLGTEIIENAVE
FILRSMSRSTGFMEFDDNEGKHSSK

FIGURE 102

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAGCCAGTCCCCAGCGGAAGCACAGCT
CAGAGCTGGTCTGCCATGGACATCCTGGTCCCACTCCTGCAGCTGCTGGTGCTGCTTCTTAC
CCTGCCCTGCACCTCATGGCTCTGCTGGCTGGCAGCCCCGTGCAAAAGCTACTTCC
CCTACCTGATGGCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAACGGAG
CTCTTCAGCCAGATAAAGGGGCTTACAGGAGCCTCCGGAAAGTGGCCCTACTGGAGCTGGG
CTGCGGAACCGGAGCCAACTTCAGTTCTACCCACCAGGCTGCAGGGTCACCTGCCTAGACC
CAAATCCCCACTTGAGAAGTTCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATAT
GAGCGGTTTGTGGTGGCTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGT
GGTGGTCTGCACTCTGGTGGCTGTGCCTGTGCAGAGCCCAAGGAAGGTCTGCAGGAGGTCC
GGAGAGTACTGAGACCAGGAGGTGTGCTCTTTCTGGAGCATGTGGCAGAACCATATGGA
AGCTGGGCCTTCATGTGGCAGCAAGTTTCAGGCCACCTGAAACACATTGGGATGGCTG
CTGCCTCACCAAGAGAGACCTGGAAGGATCTTGAGAACGCCAGTTCTCGAAATCCAATGG
AACGACAGCCCCCTCCCTGAAGTGGTACCTGTTGGCCCCACATCATGGAAAGGCTGTC
AAACAATCTTCCAAGCTCCAAGGCACCTTGCTCCTCCCCAGCCTCCAATTAGAACAA
AGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACCTAGCAGAACATGAGAGAACATT
CATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGCAATCTCTAACTCAATC
CCGCCTTCGACAGTGAAAAGCTACTTCTACGCTGACCCAGGGAGGAAACACTAGGACCC
TGTTGTATCCTCAACTGCAAGTTCTGGACTAGTCTCCCAACGTTGCCTCCAAATGTTGTC
CCTTCCTCGTCCATGGTAAAGCTCCTCGCTTCCTGAGGCTACACCCATGCGT
CTCTAGGAACCTGGTCACAAAGTCATGGTGCCCTGCATCCCTGCCAAGCCCCCTGACCCCTCT
CTCCCCACTACCACCTTCTCCTGAGCTGGGGCACCAGGGAGAATCAGAGATGCTGGGAT
GCCAGAGCAAGACTCAAAGAGGCAGAGGTTTGTCTCAAATATTTTAATAAATAGACGA
AACCACG

FIGURE 103

MDILVPLLQLLVLLTLPLHLMALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELFSQI
KGLTGASGKVALLELGCGTGANFQFYPPGCRVTCLDPNPHFEKFLTKSMAENRHLQYERFVV
APGEDMRQLADGSMDVVVCTLVLCSVQSPRKVLQEVRRLRPGGVLFFWEHVAEPYGSWAFM
WQQVFEPTWKHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWLPGPHIMGKAVKQSFP
SSKALICSFPSLQLEQATHQPIYLPLRGT

FIGURE 104

GTGGGATTTATTCAGTGAAAGATCGTTCTCAGTGGTGGGAAGTGCCTCATCGCAGG
 CAGATGTTGGGCTTGTCCGAACAGCTCCCTCTGCCAGCTCTGTAGATAAGGGTTAAA
 ACTAATATTTATATGACAGAAGAAAAAG**ATG**TCACTCCGTAAAGTAAACATCATCATCTTGG
 TCCTGGCTGTTGCTCTCTTACTGGTTGCACCATAACTCCTCAGCTTGAGCAGTTG
 TTAAGGAATGAGGTTACAGATTAGGAATTGTAGGGCTAACCTATAGACTTTGTCCCAA
 TGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCCGTGGTCATCGCTGCATCTG
 AAGACAGGCTGGGGGGCCATTGCAGCTATAAACAGCATTGACACAACACTCGCTCCAAT
 GTGATTTCTACATTGTTACTCTCAACAATACAGCAGACCATCTCCGGCTGGCTAACAG
 TGATTCCTGAAAAGCATCAGATACAAAATTGTCATTGACCTAAACTTTGGAAGGAA
 AAGTAAAGGAGGATCCTGACCAGGGGAATCCATGAAACCTTAACCTTGCAAGGTTCTAC
 TTGCCAATTCTGGTCCCAGCGAAAGAAGGCCATATACATGGATGATGATGAAATTGTGCA
 AGGTGATATTCTGCCCTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTTCA
 AAGATTGTGATTGCCTACTAAAGTTGTCATCCGTGGAGCAGGAAACCAGTACAATTAC
 ATTGGCTATCTTGACTATAAAAGGAAAGAATTGTAAGCTTCCATGAAAGCCAGCACTTG
 CTCATTAACTCTGGAGTTTGCAACACTGACGGAAATGAAACGACAGAATATAACTA
 ACCAACTGGAAAATGGATGAAACTCAATGTAGAAGAGGGACTGTATAGCAGAACCTGGCT
 GGTAGCATCACAAACACCTCTGCTTATCGTATTTTATCACAGCACTCTACCATCGATCC
 TATGTGGAATGTCCGCCACCTTGGTCCAGTGCTGGAAAACGATATTCACCTCAGTTGAA
 AGGCTGCCAAGTTACTCCATTGGAATGGACATTGAAGCCATGGGAAGGACTGCTTCATAT
 ACTGATGTTGGAAAAATGGTATATTCCAGACCCAACAGGCAAATTCAACCTAACCGAAG
 ATATACCGAGATCTCAAACATAAAG**TGA**AACAGAATTGAACTGTAAGCAAGCATTCTCAG
 GAAGTCCTGGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTCAATGCCTATCGGT
 GCAAGCCATGGAAAAGATGTGTCAGCTAGGTAAAGATGACAAACTGCCCTGTGGCAGTC
 AGCTTCCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCCTACCAAGTGTGTTCTT
 ACTACAATGCTGAATGACTGGAAAGAAGAACTGATATGGCTAGTTAGCTAGCTAGCTGGTACAGA
 TAATTCAAAACTGCTGTTGGTTAATTTGTAACCTGTGGCCTGATCTGTAATAAAACTT
 ACATTTTC

FIGURE 105

MSFRKVNIILVLAVALFLLVLHHNFLSLSLLRNEVTDGIVGPQPIDFVPNALRHAVDGR
QEEIPVIAASEDRLGGAIAAINSIQHNTRSNVIFYIVTLNNTADHLRSWLNSDSLKSIRYK
IVNFDPLLEGKVKEPDQGESMKPLTFARFYLPILVPSAKKAIYMDDDVIVQGDILALYNT
ALKPGHAAAFSEDCDSASTKVVIRGAGNQNYIGYLDYKKERIRKLSMKASTCSFNPGVFVA
NLTEWKRQNITNQLEKWMKLNVEEGLYSRTLAGSITTPPLLIVFYQQHSTIDPMWNVRHLGS
SAGKRYSPQFVKAAKLLHWNGHLKPWGRTASYTDVWEKWYIPDPTGFNLIRRYTEISNIK

FIGURE 106

TGGTTTTGCCCATAAATTCCCTCAGCTTGAGCAGTTGTTAAGGAATGAGGTTACAGATT
CAGGAATTNTAGGN CCTCAACCTNTAGANTTGTCCCAAATGTTCTCCGACATGCAGTAGAT
GGGAGACAAGAGGAGATT CCTGTGGTCATCGCTGCATNTGAAGACAGGCTGGGGGGCCAT
TGCAGCTATAAACAGCATT CAGCACAACACTCGNTCCAATGTGATTTCTACATTGTTACTC
TCAACAATACAGCAGACCNTCCGGTCCTGGNTCAACAGTGATTCCCTGAAAAGCATCAGA
TACAAAATTGTCAATT TGACCCTAAACTTTGGAAGGAAAAGTAAAGGAGGATCCTGACCA
GGGGGAATCCATGAAACCTTAACCTTGCAAGGTTCTACTTGCCAATTCTGGTCCCAGCG
CAAAGAAGGCCATATACATGGATGATGTAATTGTGCAAGGTGATATTCTGCCCTTAC
AATACAGCACTGAAGCCAGGACATGCAGCTGCATTTCAGAAGATTGTGATT CAGCCTCTAC
TAAAGTTGTCA TCCGTGGAGCAGGAAA

FIGURE 107

CGACGCTCTAGCGGTTACCGCTGCAGGGCTGGCTGGCGTAGTGGGCTGCGCGGCTGCCACG
 GAGCTAGAGGGCAAGTGTGCTCGGCCAGCGTCAGGGAACGCAGGGCGGCCAGACAACGGC
 TGGGCTCCGGGCCTGCAGGGCGGGCGTAGCTGGCAGGGCGGGTGGGGCGGGCTGCA
 TCCGCATCTCCTCCATCGCCTGCAGTAAGGGCGGCCGGCGAGCCTTGAGGGAACGACT
 TGTCGGAGCCCTAACCAAGGGGTGTCTCTGAGCCTGGTGGATCCCCGGAGCGTCACATCACT
 TTCCGATCACTCAAAGTGGTAAAAACTAATATTATATGACAGAACAGAAAAGATGTCATT
 CCGTAAAGTAAACATCATCATCTTGGCCTGGCTGTTGCTCTTCTTACTGGTTTGAC
 CATAACTCCTCAGCTGAGGCAGTTGTTAAGGAATGAGGTTACAGATTAGGAATTGTA
 GGCCTCAACCTATAGGACTTGTCCAAATGCTCTCCGACATGCAGTAGATGGAGACAAGA
 GGAGATTCTGTGGTCATCGCTGCATCTGAAGACAGGCTGGGGGGCATTGCAGCTATAA
 ACAGCATTCACTGACAACACTCGCTCCAATGTGATTTCTACATTGTTACTCTAACAAATACA
 GCAGACCATCTCCGGCCTGGCTCAACAGTGATTCCCTGAAAAGCATCAGATAACAAATTG
 TCAATTGACCCCTAAACTTTGGAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGAATCC
 ATGAAACCTTAACCTTGCAAGGTTACTTGCAATTCTGGTTCCCAGCGCAAAGAAGG
 CCATATACATGGATGATGATGTAATTGCAAGGTGATATTCTGCCCTTACAATACAGCA
 CTGAAGCCAGGACATGCAGCTGCATTTCAGAAGATTGATTGACTCTAACAGTTGT
 CATCCGGAGCAGGAAACCACTGACAATTACATTGGCTATCTTGACTATAAAAGGAAAGAA
 TTCGTAAGCTTCCATGAAAGCCAGCAGTGCTCATTAATCCTGGAGTTTGTGAAAC
 CTGACGGAATGGAAACGACAGAACATAACTAACCAACTGGAAAAATGGATGAAACTCAATGT
 AGAAGAGGGACTGTATAGCAGAACCCCTGGCTGGTAGCATCACACACCTCCTGCTTATCG
 TATTATCAACAGCACTTACCATCGATCCTATGTGGAATGTCGCCACCTGGTTCCAGT
 GCTGGAAAACGATATTCAACCTCAGTTGAAAGGCTGCCAAGTTACTCCATTGGAATGGACA
 TTTGAAGCCATGGGAAGGACTGCTCATATACTGATGTTGGGAAAATGGTATATTCCA
 GACCCAAACAGGCAAATTCAACCTAACCGAAAGATACCGAGATCTCAAACATAAAGTGA
 CAGAATTGAACTGTAAGCAAGCATTCTCAGGAAGTCCTGGAAAGATAGCATGCGTGGAAAG
 TAACAGTTGCTAGGCTCAATGCCTATCGGTAGCAAGCCATGGAAAAGATGTGTCAGCTAG
 GTAAAGATGACAAACTGCCCTGTCTGGCAGTCAGCTCCAGACAGACTATAGACTATAAAT
 ATGTCCTCATCTGCCATTACCAAGTGTGTTACTACAATGCTGAATGACTGGAAAGAAGAA
 CTGATATGGCTAGTTCAGCTAGCTGGTACAGATAATTCAAAACTGCTGTTGGTTAATT
 GTAACCTGTGGCCTGATCTGAAATAAAACTACATTTCATAGGTAAAAAAAAAAAAAA
 AAAAAA

FIGURE 108

CTGCAGGTAGACATCTCACTGCCAGGAATCACTGAGCGTGAGACAGCACAGCCTCCT
GAAGGCCGGCCATACCAGAGTCCTGCCTCGGCATGGGCCTCACCATTGAGGCAGCTCCACTG
TCTGTGCTGGTCTGAGGGTGTGCCTGTCATGGGGGCAGCCATCTCCCAGGGGCCCTCATC
GCCATCGTCTGCAACGGTCTCGTGGCTTCTGCTGCTGCTCTGGTCATCCTCTGCTG
GGCCTGCCATTCTCGTCTGCCGACGTTGACTCTCTCTGAATCCAGTCCAACCTCCAGCCC
TGGCCCCCTGTCCTGAGAAGGCCACCACCCAGAACGCCAGCCATGAAGGCAGCTACCTGC
TGCAGCCCTGAAGGCCCTGGCCTAGCCTGGAGCCCAGGACCTAAGTCCACCTCACCTAGAG
CCTGGAATTAGGATCCCAGAGTTAGCCAGCCTGGGTCCAGAACTCAAGAGTCCGCCTGCT
TGGAGCTGGACCCAGCGGCCAGAGTCTAGCCAGCTGGCTCCAATAGGAGCTCAGTGGCCC
TAAGGAGATGGCCTGGGTGGGGCTTATGAGTTGGTGTAGAGCCAGGGCCATCTGGACT
ATGCTCCATCCAAGGGCAAGGGTCAGGGCCGGTCCACTCTTCCTAGGCTGAGCACC
TCTAGGCCCTTAGGTTGGGAAGCAAACGGAACCCATGGCAATAATAGGAGGGTGTCCAG
GCTGGCCCCCTCCCTGGCCTCCAGTGTGCTGGATAATAATGGAACATGGCTCTAA
AAAAAAAAAAAAAAA

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FIGURE 109

MGAAISQGALIAIVCNGLVGFLLLLWVILCWACHSRLPTLTLNPVPTPALAPVLRRPHH
PRSPAMKAATCCSPEGPWPSLEPRT

FIGURE 110

GTTTGAATTCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGGCTACCA
 GTTCCTCCAAGCAAGTCATTCCCTTATTAACCGATGTGTCCCTCAAACACCTGAGTGCTA
 CTCCCTATTGCATCTGTTGATAAAATGATGTTGACACCCTCCACCGAATTCTAAGTGGAA
TCATGTCGGGAAGAGATAACAATCCTGGCCTGTGTATCCTCGCATTAGCCTTGTCTTGGCC
 ATGATGTTACCTCAGATTCATCACCAACCCTCTGGTTCACATTTCATTTCATTGGTTAT
 TTTGGGATTGTTGTTGTCTGCGGTGTTATGGTGGCTGTATTATGACTATACCAACGACC
 TCAGCATAGAATTGGACACAGAAAGGGAAAATATGAAGTGCCTGCTGGGGTTGCTATCGTA
 TCCACAGGCATCACGGCAGTGCTCGTCTGATTGTTCTCAGAAAGAGAATAAAATT
 GACAGTTGAGCTTTCAAATCACAAATAAGCCATCAGCAGTGCTCCCTGCTGTTCC
 AGCCACTGTGGACATTGCCATCCTCATTCTCTGGTCCTCTGGTGGCTGTGCTGCTG
 AGCCTGGGAACACTCAGGAGCTGCCAGGTTATGGAAGGCGGCCAAGTGGAATATAAGCCCCT
 TTCGGGCATTGGTACATGTGGTGTACCTTAATTGGCCTCATCTGGACTAGTGAATTCA
 TCCTTGCCTGCCAGCAAATGACTATAGCTGGGCAGTGGTTACTGTTATTCACAGAAAGT
 AAAAATGATCCTCCTGATCATCCCATTCTCGTCTCTCCATTCTTCTTACCATCA
 AGGAACCGTTGTGAAAGGGTCATTTAATCTCTGTGGTGTGAGGATTCCGAGAACATTGTCA
 TGTACATGCAAAACGCACTGAAAGAACAGCAGCAGCATGGTGCATTGTCCAGGTACCTGTTCCGA
 TGCTGCTACTGCTGTTCTGGTGTCTGACAAATACCTGCTCCATCTCAACCAGAACATGCATA
 TACTACAACGTCTATTAAATGGGACAGATTCTGTACATCAGCAAAGATGCATTCAAATCT
 TGTCCAAGAAACTCAAGTCACTTACATCTATTAACTGCTTGGAGACTTCATAATTCTCA
 GGAAAGGTGTTAGTGGTGTGTTCACTGTTGGAGGACTCATGGCTTTACTACAATCG
 GGCATTCCAGGTGTGGCAGTCCCTCTGTTATTGGTAGCTTTGCCTACTTAGTGGCCC
 ATAGTTTTATCTGTGTTGAAACTGTGCTGGATGCACCTTCCTGTGTTGCTGTTGAT
 CTGGAAACAAATGATGGATCGTCAGAAAAGCCCTACTTATGGATCAAGAACATTCTGAGTT
 CGTAAAAAGGAGCAACAAATTAAACAAATGCAAGGGCACAGCAGGACAAGCACTCTTAAAGGA
 ATGAGGAGGGAACAGAACTCCAGGCCATTGTGAGA**TAG**ATACCCATTAGGTATCTGTACCT
 GGAAAACATTCCCTCTAAGAGCCATTACAGAAATAGAAGATGAGACCCTAGAGAAAAGTT
 AGTGAATTTTTTAAAAGACCTAATAAACCCATTCTTCTCAAAA

FIGURE 111

MSGRDTIILGLCILALALSLAMMFTFRFITTLLVHIFISLVLGLLFVCGVLWWLYDYTN
SIELDTERENMKCVLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPFL
PLWTFAILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFI
LACQQMTIAGAVVTCYFNRSKNDDPDPHPILSSLSILFFYHQGTVVKGSLISVVRIPRIIVM
YMQNALKEQQHGALSRYLFRCYCFCWCLDKYLLHQNAYTTAINGTDFCTSAKDAFKIL
SKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAFQVWAVPLLLVAFFAYLVAH
SFLSVFETVLDALFLCAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRN
EEGTELQAIVR

FIGURE 112

GTTCGATTAGCTCCTCTGAGAAGAAGAAAAGGTTCTGGACCTCTCCCTGTTCTCCCT
 AGAATAATTGTATGGGATTGTGATGCAGGAAAGCTAACGGAAAAAGAATATCATTCTG
 TGTGGTAAAATTGGAAAAAAATTGCCTCTTCAAACAAGGGTGTCAATTGTGATATT
TATGAGGACTGTTCTCACTATGAAGGCATCTGTATTGAAATGTTCTGTTGCTGG
 TGACTGGAGTACATTCAAACAAAGAAACGGAAAGAAGATTAAAAGGCCAAGTCACTGTG
 CCTCAGATCAACTGCATGTCAGGCCAAAGATCATCGATCCTGAGTTCAATTGTGAAATG
 TCCAGCAGGATGCCAACGACCCAAATACATGTTATGGCACTGACGTGTATGCATCCTACT
 CCAGTGTGTGCGCTGCCGTACACAGTGGTGTGCTGATAATTCAAGGGAAAATACCT
 GTTCGGAAGGTTGCTGGACAGTCTGGTTACAAAGGGAGTTATTCACGGGTGTCACATGTT
 ATCCCTACCACGATGGAGAGAATCCTTATCGTCTTAGAAAGTAAACCAAAAGGGTGTAA
 CCTACCCATCAGCTCTACATACATCGAAAAGTCCAGCTGCCAACGAGGTGAGACC
 ACACAAAGCCTATCAGAGGCCACCTATTCCAGGGACAACTGACAGCCGGTCACTGTATGCA
 GCTTCTGGCTGTCACTGTAGCTGGCCACCCCCACCCACCTGCCAACGCCATCCCCTCTG
 CTGCTTCTACCACCAACGATCCCCAGACCACAATCAGTGGGCCACAGGAGCCAGGAGATGGAT
 CTCTGGTCCACTGCCACCTACACAAGCAGCCAAACAGGCCAGAGCTGATCCAGGTATCCA
 AAGGCAAGATCCTCAGGGAGCTGCCCTCCAGAAACCTGTTGGAGCGGATGTCAGCCTGGGAC
 TTGTTCCAAAAGAAGAATTGAGCACACAGTCTTGGAGGCCAGTATCCCTGGGAGATCCAAC
 TGCAAAATTGACTGTCGTTTAATTGATGGGAGCACCAGCATGGCAACAGGGGATTCCG
 AATCCAGAAGCAGCTCCTGGCTGATGTTGCCAAGCTTGCACATTGGCCCTGCCGTCAC
 TGATGGGTGTTGTCAGTATGGAGACAACCTGCTACTCACTTAACCTCAAGACACACACG
 AATTCTCGAGATCTGAAGACAGCCATAGAGAAAATTACTCAGAGAGGAGGACTTCTAATGT
 AGGTGGGCCATCTCCTTGTGACCAAGAACCTCTTCCAAAGCCAATGGAAACAGAACG
 GGGCTCCAATGTGGTGGGGTGTGGGGATGGCTGGCCACGGACAAAGTGGAGGAGGCT
 TCAAGACTTGCAGAGAGACTGAGGAATCAACATTTCATCACCATTGAAGGTGCTGCTGA
 AAATGAGAAGCAGTATGTGGTGGAGGCCAACCTTGCAAACAAGGCCGTGTCAGAACAAACG
 GCTTCTACTCGCTCACGTGCAGAGCTGGTTGGCCTCCACAAGACCCCTGCAGCTCTGGT
 AAGCGGGTCTGCACACTGACCGCCTGCCCTGCAGCAAGACCTGCTGAACTCGGCTGACAT
 TGGCTTCTGTCATCGACGGCTCCAGCAGTGTGGGGAGGGCAACTCCGCACCGCTCCAGT
 TTGTCACCAACCTCACAAAGAGTTGAGATTTCGACACGGACAGCGCATCGGGCCGTG
 CAGTACACCTACGAACAGCGGCTGGAGTTGGGTGACAAAGTACAGCAGCAAGCCTGACAT
 CCTCAACGCCATCAAGAGGGTGGCTACTGGAGTGGTGGCACAGCACCGGGCTGCCATCA
 ACTTCGCCCTGGAGCAGCTTCAAGAAGTCAAGGCCAACAGAGGAAGTTAATGATCC
 ATCACCGACGGGAGGTCTACGACGACGTCCGGATCCAGCCATGGCTGCCCATCTGAAGGG
 AGTGTACACCTATGCGATAGGCCTGGCTGCCAACAGAGGAGCTAGAAGTCATTGCCA
 CTCACCCGCCAGAGACCACCTCTTGTGGACGAGTTGACAACCTCCATCAGTATGTC
 CCCAGGATCATCCAGAACATTGTACAGAGTTCAACTCACAGCCTCGGAAC**TGA**ATTGAG
 CAGGCAGAGCACCAGCAAGTGTGCTTACTAAGTGCAGTGTGGACCACCCACCGCTTAA
 TGGGGCAGCAGCAGGTGCATCAAGTCTGGCAGGGCATGGAGAAACAAATGTCTGTTATT
 TTCTTGCCATCATGCTTTCATATTCAAACCTGGAGTTACAAAGATGATCACAAACGT
 ATAGAATGAGCCAAAGGCTACATGTTGAGGGTGTGGAGATTTCACATTGACAATT
 GTTTCAAAATAATGTTGGAATACAGTGCAGCCCTACGACAGGCTACGTAGAGCTTT
 GTGAGATTGTTAAGTGTATTGATTTGAACTCTGTAACCTCAGCAAGTTCAATT
 GTCATGACAATGTAGGAATTGCTGAATTAAATGTTAGAAGGATGAAAATAAAAAAAAA
 AAAG

FIGURE 113

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINC DVKAGKIIDPEFIVKC
PAGCQDPKYH VY GTDVY ASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQL
SLPRWRESFIVLESKP KKGVTYPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMQ
LLAVTVAVATPTTLP RPSPSA STTSI PRPQSVGHRSQEMDLWSTATYTSSQNRPRADPGIQ
RQDPSGAAFQKPVGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFR
IQKQLLADVAQAL DIGPAGPLMGVVQYGDNPATHFNLKHTNSRDLKTAIEKITQRGGLSNV
GRAISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAE
NEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKTIQPLVKRVCDTRLACSKTCLNSADI
GFVIDGSSSVGTGNFRTVLQFVTNLTKFEISDTDTRIGAVQTYEQRLEFGFDKYSSKPDI
LNAIKR VGYWSGGTSTGAAINFALEQLFKKS KPNKRKLMILITDGRSYDDVRI PAMA AHLKG
VITYAIGVAWAQAEELEVIATHPARDHSFFVDEFDNLHQYVPRI IQNICTEFNSQPRN

FIGURE 114

CAGGATGAACCTGGTTGCAGTGGCTGCTGCTGCGGGGGCGCTGAGAGGGACACGAGCTCTA
TGCCTTCGGCTGCTCATCCGCTCGGCCTCCTGTGCGCGCTGCTGCCTCAGCACCATGGT
 GCGCCAGGTCCCACGGCTCCGCGCCAGATCCGCCCACTACAGTTTCTCTGACTCTAAAT
 TGATGCACGGACACCTTGCTGATTGGAAATGTCTCAGAATTCAAAGAGTGGTTGAAG
 TGCTCCAGGACAGCGTGGACTTGATATTGATGTGAACGCCTCTGTGTTGAAACAAACATT
 CGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGGCTGGGTGGAAGTAGA
 GGCTGGATGGCCCTGTTCCGGCCTCTCCTGAGAATGGCTGAGGAGGCAGCCGAAACTCC
 TCCCAGCCTTCAGACCCCCACTGGCATGCCATATGAAACAGTGAACTTACTTCATGGCGTG
 AACCCAGGAGAGACCCCTGTCACCTGTACGGCAGGGATTGGGACCTTCATTGTTGAATTGC
 CACCCCTGAGCAGCCTCACTGGTGACCCGGTGTCAAGATGTGCCAGAGTGGCTTGATGC
 GCCTCTGGAGAGCCGGTCAGATATCGGGCTGGTCGCAACCACATTGATGTGCTCACTGGC
 AAGTGGGTGGCCCAGGACGCCAGGCATGGGCTGGCTGGACTCCTACTTGAGTACTGGT
 GAAAGGAGCCATCCTGTTCAAGATAAGAACGCTATGCCATGTTCTAGAGTATAACAAAG
 CCATCCGGAACTAACCCGCTTCGATGACTGGTACCTGTGGTTCAAGATGTACAAGGGACT
 GTGTCCATGCCAGTCTCCAGTCCTGGAGGCCTACTGGCCTGGCTTCAGAGCCTCATTGG
 AGACATTGACAATGCCATGAGGACCTTCCTCAACTACTACACTGTATGGAAGCAGTTGGG
 GGCTCCCGAATTCTACAACATTCCCTCAGGGATAACAGTGGAGAAGCGAGAGGGCTACCC
 CCTCGGCCAGAACTTATTGAAAGCGCAATGTACCTCTACCGTGCACGGGGATCCACCC
 CCTAGAACTCGGAAGAGATGCTGTGGAATCCATTGAAAAAAATCAGCAAGGTGGAGTGC
 TTGCAACAATCAAAGATCTGCGAGACCACAAGCTGGACAACCGCATGGAGTCGTTCTC
 GCCGAGACTGTGAAATACCTCTACCTCCTGTTGACCAACCAACTTCATCCACAACAA
 GTCCACCTTCGACCGGGTGTACCCCCCTATGGGAGTGCATCCTGGGGCTGGGGTACA
 TCTTCAACACAGAAGCTCACCCATCGACCTGCCGCCCTGCACTGCTGCCAGAGGCTGA
 GAAGAGCAGTGGAGGTGGAGGAATTCTACTCTCTCAAACGGAGCAGGTC
 GAAATTTCAGAAAAACACTGTTAGTTGGGCCATGGAACCTCCAGCAAGGCCAGGAACAC
 TCTTCTCACCAGAAAACCATGACCAGGCAAGGGAGAGGAAGCCTGCCAACAGAAAG
 GTCCCTAGCTGCCAGTCAGCCCTCACCTCCAAGTTGGCATTACTGGGACAGGTTTC
 AGACTCCTCATAACCACTGGATAATTTTTATTTTTGAGGCTAAACTATAATA
 AATTGCTTTGGCTATCATAAAA

FIGURE 115

MPFRLLIPLGLLCALLPQHHGAPGPDSAPDPAHYSFSLTLIDALDTLLILGNVSEFQRVVE
VLQDSVDFIDVNASFETNIRVVGGLL SAHLLSKKAGVEVEAGWPCSGPLL RMAEEAARKL
LPAFQTPTGMPYGTVNLLHGVPGETPVTCTAGIGTFIVEFATLSSLTGDPVFEDVARVALM
RLWESRSDIGLVGNHIDVLTGKWVAQDAGIGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNK
AIRNYTRFDDWYLWVQMYKGTVSMPVFQSLEAYWPGLQSLIGDIDNAMRTFLNYYTWKQFG
GLPEFYNI PQGYTVEKREGYPLRPELIESAMYLYRATGDPTLLELGRDAVESIEKISKVECG
FATIKDLRDHKLDNRMESFFLAETVKYLYLLFDPTNFIHNGSTFDAVITPYGECILGAGGY
IFNTEAHPIDLAALHCCQRLKEE QWEVEDLMREFYSIKRSRSKFQKNTVSSGPWEPPARPGT
LFSPENHDQARERKPAKQKVPLLSCPSQPFTSKLALLGQVFLDSS

FIGURE 116

AAAGTTACATTTCTCTGGAACCTCCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTG
 GGCAGAAAGGAGGGTGCTTCGGAGCCGCCCTTCTGAGCTCCTGGGCCGGCTAGAACAA
 ATTCAAGGCTTCGCTGCGACTCAGACCTCAGCTCAAACATATGCATTCTGAAGAAAGATGGCT
 GAGATGGACAGAATGCTTATTTGAAAGAACAAATGTTCTAGGTCAAACGTGAGTCTACCA
AATGCAGACTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTCATGTGGTTTCT
 ACGCATTGATTCCATGTTGCTCACAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTC
 TCTGTACTCTCAACCAACATGAAGCATCTTGTGATGTGGAGCCAGTGATCGCGCTGGAGA
 AACAGTGTACTATTCTGTCGAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
 GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCTGAGTGTGATGTCAGTGACATC
 ACGGCCACTGTGCCATAAACCTCGTGTCAAGGCCACATTGGCTCACAGACCTCAGCCTG
 GAGCATTCTGAAGCATTCCCTTAATAGAAACTCAACCACCTTACCCGACCTGGATGGAGA
 TCACCAAAGATGGCTCCACCTGGTTATTGAGCTGGAGGACCTGGGCCAGTTGAGTTC
 CTTGTGGCTACTGGAGGAGGGAGCCTGGTGCCAGGAACATGTCAAAATGGTGAGGAGTGG
 GGGTATTCCAGTGCACCTAGAAACCATGGAGCCAGGGCTGCATACTGTGTGAAGGCCAGA
 CATTCTGAAGGCCATTCCCCTGGTACTGCCCTGTTGCCTTGGCTCATGCTGATCCTGT
 GGTGTCGCACTGTTGTCGGAAAATGGCCGGCTGCTCCAGTACTCCTGTTGCCCGTGG
 TGGTCCTCCCAGACACCTGAAAATAACCAATTACCCCCAGAAGTTAACAGCTGAGAAGG
 GAGGAGGTGGATGCCCTGTGCCACGGCTGTGATGTCCTGAGGAACCTCCTCAGGGCTGGAT
 CTCA**TAG**TTGCGGAAGGGCCAGGTGAAGCCGAGAACCTGGCTGCATGACATGGAAACC
 ATGAGGGACAAGTTGTGTTCTGTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA
 GCCTGTTGCTACAAGTCTAGAACCAACCATCAGAGGCAGGGTGGTTGTCTAACAGAACAC
 TGACTGAGGCTTAGGGATGTGACCTCTAGACTGGGGCTGCCACTGCTGGCTGAGCAACC
 CTGGAAAAGTGACTTCATCCCTCGGTCTAACGTTCTCATCTGTAAATGGGAAATTACC
 TACACACCTGCTAAACACACACACAGAGTCTCTCTATATACACACGTACACATAAA
 TACACCCAGCACTGCAAGGCTAGAGGGAAACTGGTGACACTACAGTCTGACTGATTGAG
 TGTGTTCTGGAGAGCAGGACATAATGTATGATGAGAACATGATCAAGGACTCTACACACTGGG
 GGCTTGGAGAGCCCACTTCCCAGAATAATCCTTGAGAGAAAAGGAATCATGGAGCAATGG
 TGTTGAGTTCACTTCAAGCCCAATGCCGGTGCAGAGGGAAATGGCTTAGCGAGCTCTACAGT
 AGGTGACCTGGAGGAAGGTACAGCCACACTGAAAATGGGATGTGCATGAACACGGAGGATC
 CATGAACACTGTAAAGTGTGACAGTGTGACACTGCAGACAGCAGGTGAAATGTATGT
 GTGCAATGCGACGAGAACATGCAGAACAGTCAGTAACATGTGCATGTTGTTGCTCCTTTTC
 TGTTGGTAAAGTACAGAACATAAAAGGGCCACCCTGGCAAAAGCGGTAAAAAA
 AAAAAAA

FIGURE 117

MQTFTMVLEEIWTSLFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLLMWSPVIAPGE
TVYYSVYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDDITATVPYNLRVRATLGSQTSAW
SILKHPFNRNSTILTRPGMEITKDGFLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSG
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPLVLALFAFVGFMLILV
VVPLFVWKMGRLLQYSCCPVVLPDTLKINTSPQKLISCRREEVDACATAVMSPEELLRAWIS

Important features:

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation sites.

amino acids 40-43 and 134-137

Tissue factor proteins homology.

amino acids 92-119

Integrins alpha chain protein homology.

amino acids 232-262

FIGURE 118

TCCTGCTGATGCACATCTGGTTGGAAAAGGAGGTTGCTCGAGCCGCCCTTAGCTT
CCTGGCCGGCTCTAGAACATTAGGCTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTATTTGAAAGAAACAATGTTCTAGG
TCAAAATGAGTCTACCAAATGCAGACTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT
TTTCATGTGGTTTCTACGCATTGATTCCATGTTGCTCACAGATGAAGTGGCATTCTGC
CTGCCCTCAGAACCTCTGTACTCTAACCAACATGAAGCATCTTGATGTGGAGCCA
GTGATCGCGCTGGAGAACAGTGTACTATTCTGTCGAATACCAGGGGAGTACGAGAGCCT
GTACACGAGGCCACATCTGGATCCCCAGCAGCTGGTCACTCACTGAAGGTCTGAGTGTG
ATGTCACTGATGACATCACGGCCACTGTGCCATACAAACCTTGTCAGGGCACATTGGC
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTAATAGAAACTCAACCATTCTAC
CCGACCTGGATGGAGATACCAAAGATGGCTNCACCTGGTTATTGAGCTGGAGGACCTGG
GGCCCCAGTTGAGTTCTGTGGCTANTGGAGGAGGGCGAACCCCTGCGCGCAAGGG
GTTNGCGAACCCCTTGCAGGCCGCTGGGTATCTCTCGAGAAAAGAGAGGCCAATATGACCCAC
ATACTCAATATGGACGAANTGCTATTGTCCACCTGTTGAGTGGCGCTGGGTGAT

FIGURE 119

CGGACGCGTGGGCCAACCTCCGAACAAGCC**ATG**GTGGCGGCACGGTGGCAGCGCGTG
GCTGCTCCTGTGGGCTGCGGCTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGGC GG
TCAACATCCGGGGCAAACCTGGTGTGCGCTGGAGAAGTACCGCGGATCGGTGTCCTGGTGGTG
AATGTGGCCAGCGAGTGC GGCTTCACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCG
AGACCTGGGCCCCCACCACCTTAACGTGCTCGCCTCCCCTGCAACCAGTTGGCCAACAGG
AGCCTGACAGCAACAAGGAGATTGAGAGCTTGCCCGCCGACCTACAGTGTCTCATTCCCC
ATGTTAGCAAGATTGCAGTCACCGGTACTGGTGCCCATCCTGCCTCAAGTACCTGGCCA
GACTTCTGGGAAGGAGCCCACCTGGAACTTCTGGAAGTACCTAGTAGCCCCAGATGGAAAGG
TGGTAGGGGCTTGGGACCCA ACTGTGTCA GTGGAGGAGGT CAGACCCAGATCACAGCGCTC
GTGAGGAAGCTCATCCTACTGAAGCGAGAAGACTTA**TAA**CCACCGCGTCTCCTCCACCA
CCTCATCCGCCACCTGTGTGGGCTGACCAATGCAAACCTCAAATGGTGTCAAAGGGAG
AGACCCACTGACTCTCCTCTTACTCTTATGCCATTGGTCCATCATTGTGGGGGAA
AAATTCTAGTATTTGATTATTGAATCTTACAGCAACAAATAGGAACCTCCTGGCCAATGAG
AGCTCTTGACCAGTGAATCACCA CGCGATA CGAACGTCTGCCAACAAAATGTGTGGCAA
TAGAA GTATATCAAGCAATAATCTCCACCCAGGCTCTGTAAACTGGGACCAATGATTAC
CTCATAGGGCTGTGTGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGC
CAAATAGGAGGCATTCAATGAACATTGGCATATAACCAAAAAATAACTGTGTATCAAT
AAAAACTGCATCCAACATGAATTCCAGCCGATGATAATCCAGGCCAAAGGTTAGTTGTT
GTTATTTCTCTGTATTATTTCTCATTACAAAAGAAATGCAAGTTCATTGTAACAATCCA
AACAACTCACGATATAAAATGAAAGTATCCTCCTCAAAA

FIGURE 120

MVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGKLVSLEKYRGSVSLVVNVASECGFTDQ
HYRALQQLQRDLGPHHFNVLAFCNCQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTG
AHPAFKYLAQTSGKEPTWNFWKYLVAPDGKVVGAWDPTVSVEVRPQITALVRKLILLKREDL

FIGURE 121

CGGACGCGTGGCGGGCCGGGACGCAGGGCAAAGCGAGCC**ATG**GCTGTCTACGTGGGATGC
 TGCCTGGGGAGGCTGTGCGCCGGAGCTGGGGTGTGGGGCCGCCCTCTCT
 CGGAGTTGGCAGGAAGCCAGGTTGCAAGGGTGTCCGCTCCTCAGTTCCAGAGAGGGTGGATCG
 CATGGTCTCCACGCCATCGGAGGCCTCAGCTACGTTCAAGGGTGCACCAAAAGCATCTTA
 ACAGCAAGACTGTGGGCCAGTGCCTGGAGACCACAGCACAGAGGGTCCCAGAACGAGAGGCC
 TTGGTCGTCCATGAAGACGTCAAGGTTGACCTTGCCCAACTCAAGGAGGAGGTGGACAA
 AGCTGCTCTGGCCTCTGAGCATTGGCCTCTGCAAAGGTGACCGGCTGGCATGTGGGAC
 CTAACCTCATGGTGCTCATGCAGTTGCCACGCCAGGGCATCATTCTGGT
 TCTGTGAACCCAGCCTACCAGGCTATGGAACGGTATGTCCTCAAGAAGGTGGCTGCAA
 GCCCTTGTGTTCCCAAGCAATTCAAGACCCAGCAATACTACAACGTCTGAAGCAGATCT
 GTCCAGAAGTGGAGAATGCCAGGCCAGGGCTTGAAGAGTCAGAGGCTCCAGATCTGACC
 ACAGTCATCTCGGTGGATGCCCTTGCAGGGACCTGCTCTGGATGAAGTGGTGGCGGC
 TGGCAGCACACGGCAGCATCTGACCTCAACACCAGCAGTTCTGTCCATGCCATG
 ACCCCATCAACATCCAGTTCACCTGGGGACAACAGGCAGCCCCAACGGGGCACCCCTCTCC
 CACTACAACATTGCAACAACATTAGGAGAGCGCTGAAACTGCATGAGAAGAC
 ACCAGAGCAGTTGGGATGATCCTGCCAACCCCTGTACCATTCGCTGGGTTCCGTGGCAG
 GCACAATGATGTGCTGATGTACGGTGCACCCCTCATCCTGGCTCTCCATCTCAATGGC
 AAGAAGGCACTGGAGGCCATCAGCAGAGAGAGAGGCACTTCTGTATGGTACCCCCACGAT
 GTTCGTGGACATTCTGAACCAGCCAGACTCTCCAGTTATGACATCTGACCATGTGTGGAG
 GTGTCATTGCTGGTCCCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAT
 ATGAAGGACCTGGGGTTGCTTATGGAACCACAGAGAACAGTCCGTGACATTCGCGCACTT
 CCCTGAGGACACTGTGGAGCAGAAGGCAGAAAGCGTGGGAGAATTATGCCCTCACACGGAGG
 CCCGGATCATGAACATGGAGGCAGGGACGCTGGCAAAGCTGAACACGCCGGGAGCTGTGC
 ATCCGAGGGTACTGCGTCATGCTGGCTACTGGGTGAGCCTCAGAACAGAGAGGAAAGCAGT
 GGATCAGGACAAGTGGTATTGGACAGGAGATGCGCCACAATGAATGAGCAGGGCTCTGCA
 AGATCGTGGCCGCTCTAAGGATATGATCATCCGGGTGGTGAGAACATCTACCCGAGAG
 CTCGAGGACTCTTACACACACCCGAAGGTGCAGGAAGTCAGGTGGTGGAGTGAAGGA
 CGATCGGATGGGAAAGAGATTGTCCTGCATTGGCTGAAGGACGGGAGGAGACCACGG
 TGGAGGAGATAAAAGCTTCTGCAAAGGAAAGATCTCACTTCAAGATTCCAAGTACATC
 GTGTTGTCACAAACTACCCCTCACCATTCAAGGAAAGATCCAGAAATTCAAACCTCGAGA
 GCAGATGGAACGACATCTAAAT**GTGA**ATAAAGCAGCAGGCCTGCTGGCGGTTGGCTT
 GACTCTCTGTCAGAATGCAACCTGGCTTATGCACCTAGATGTCCCCAGCACCCAGTTC
 TGAGCCAGGCACATCAAATGTCAAGGAATTGACTGAACGAACAAAGAGCTCCTGGATGGTC
 CGGGAACTCGCCTGGGCACAAGGTGCCAAAGGCAGGCAGCCTGCCAGGCCCTCCCTCTG
 TCCATCCCCACATTCCCTGTCCTGATTTGGCATAAAGAGCTCTGTTCTTT
 GAAAAAAA

FIGURE 122

MAVYVGMLRLGRLCAGSSGVLGARAALSRSWQEARNLQGVRFLOSSREVDRMVSTPIGGLSYVQ
GCTKKHLSKTVQOCLETTAQRVPEREALVVLHEDVRLTFAQLKEEVDKAASGLLSIGLCKG
DRLGMWGPNSYAWVLMQLATAQAGIILVSVNPAYQAMELEYVLKKVGCKALVFPKQFKTQQY
YNVLKQICPEVENAQPGALKSQRLPDLTTVISVDAPLPGTLLDEVVAAGSTRQHLDQLQYN
QQFLSCHDPINIQFTSGTTGSPKGATLSHYNIVNNNSNILGERLKLHEKTPEQLRMILPNPLY
HCLGSVAGTMMCLMYGATLILASPIFNGKKALEAISRERGTFLYGTPTMFVDILNQPDFSSY
DISTMCGGVIAGSPAPPELIRAIINKINMKDLVVAYGTTENSPVTFAHFPEDTVEQKAESVG
RIMPHTEARIMNMEAGTLAKLNTPGELCIRGYCVMLGYWGEPKTEEAVDQDKWYWTGDVAT
MNEQGFCKIVGRSKDMIIRGGENIYPAELEDFFHHPKVQEVBVGVKDDRMGEEICACIRL
KDGEETTVEEIKAFCKGKISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL

Signal Peptide:

amino acids 1-22

Transmembrane Domains:

amino acids 140-161, 213-229, 312-334

Putative AMP-binding Domain Signature:

amino acids 260-271

N-myristoylation Sites:

amino acids 19-24, 22-27, 120-125, 203-208, 268-273, 272-277,
314-319, 318-323, 379-384, 380-385, 409-413

N-glycosylation Site:

amino acids 282-285

FIGURE 123

CAACTCCAACATTAGGAGAGCGCCTGAAACTGCATGAGAAGACACCAGAGCAGTTGCGGA
TGATCCTGCCAACCCCTGTACCATTGCCTGGTTCGTGGCAGGCACAATGATGTGTCTG
ATGTACGGTGCCACCCTCATCCTGGCCTCTCCATCTCAATGGCAAGAAGGCAGTGGAGGC
CATCAGCAGAGAGAGAGGCACCTCCTGTATGGTACCCCCACGATGTTCGTGGACATTCTGA
ACCAGCCAGACTTCTCCAGTTATGACATCTGACCATGTGTGGAGGTGTCAATTGCTGGTCC
CCTGCACCTCCAGAGTTGATCCGAGGCATCATCAACAAGATAAATATGAAGGACCTGGTGGT
TGCTTATGGAACCACAGAGAACAGTCCC GTGACATT CGCG CACTT CCCTGAGGACACTGTGG
AGCAGAAGGCAGAAAGCGTGGCAGAATTATGCCTCACACGGAGGCGCGGATCATGAACATG
GAGGCAGGGACGCTGGCAAAGCTGAACACGCCGGGAGCTGTGCATCCGAGGGTACTGCGT
CATGCTGGCTACTGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGGATCAGGACAAGTGGT
ATTGGACAGGAGATGTCGCCAC

FIGURE 124

GAGCAGGACGGAGCCATGGACCCC GCCAGGAAAGCAGGTGCCAGGCCATGATCTGGACTGC
 AGGCTGGCTGCTGCTGCTGCTCGCGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCG
 TGCAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGCGCGCCGGC
 GTGGACGTCTGCACCGAGGCCGTGGGGCGGTGGAGACCATCCACGGACAATTCTCGCTGGC
 AGTGCGGGTTGCGGTTGGGACTCCCCGGCAAGAATGACCGCGGCCTGGATCTTCACGGG
 TTCTGGCGTTCATCCAGCTGCAGCAATGCGCTCAGGATCGCTGCAACGCCAAGCTAACCTC
 ACCTCGCGGCGCTCGACCCGGCAGGTAATGAGAGTGACATACCCGCCAACGGCGTGGAGTG
 CTACAGCTGTGTGGCCTGAGCCGGAGGCGTGCACGGGTACATGCCGCCGGTGTGAGCT
 GCTACAACGCCAGCGATCATGTCTACAAGGGCTGCTCGACGGCACGTCACCTGACGGCA
 GCTAATGTGACTGTGTCCCTGCCTGTCCGGGCTGTGTCCAGGATGAATTCTGCACTCGGA
 TGGAGTAACAGGCCAGGGTTCACGCTCAGTGGCTCCTGTTGCCAGGGTCCCCTGTAAC
 CTGACCTCCGCAACAAGACCTACTTCTCCCCTCGAATCCCACCCCTGTCGGCTGCCCT
 CCAGAGCCCACGACTGTGGCCTAACCACATCTGTCACCACTTACCTCGGCCAGTGAG
 ACCCACATCCACCACCAAACCCATGCCAGCGCCAACCAGTCAGACTCCGAGACAGGGAGTAG
 AACACGAGGCCTCCGGATGAGGAGCCAGGTTGACTGGAGGCCTGGCCACCGAGGAC
 CGCAGCAATTCAAGGGCAGTATCCTGCAAAAGGGGGCCCGAGCAGCCCCATAATAAGGCTG
 TGTGGCTCCCACAGCTGGATTGGCAGCCCTCTGTTGCCGTGGCTGGTGTCTACTGT
GA GCTTCTCCACCTGGAAATTCCCTCTCACCTACTTCTCTGCCCTGGTACCCCTTTCT
 CATCACTCCTGTTCCCACCACTGGACTGGCTGGCCAGGCCCTGTTCCAAACATTCCC
 CAGTATCCCCAGCTTCTGCTGCGCTGGTTGCCGCTTGGAAATAAAACCGTTGTATAT
 ATTCTGCCAGGGTGTCTAGCTTTGAGGACAGCTCTGTATCCTCTCATCCTGTCT
 TCCGCTTGTCTCTGTGATGTTAGGACAGAGTGAGAGAAGTCAGCTGTACGGGAAGGTG
 AGAGAGAGGATGCTAAGCTCCTACTCAGCTTCTCTAGCCAGCCTGGACTTGGAGCGTGG
 GGTGGGTGGACAATGGCTCCCCACTCTAACGACTGCCCTCCACTCCCCGATCTTGGG
 GAATCGGTTCCCCATATGTCTCCTACTAGACTGTGAGCTCCTCGAGGGGGGCCGGTAC
 CCAATTGCCCTATAGTGAGTCGTA

FIGURE 125

MDPARKAGAQAMIWTAGWL~~LLLLL~~RGGAQALECYSCVQKADDGCS
EAVGAVETIHGQFSLAVRGCGSGLPGKNDRGLDLHGLLAFIQLQQCAQDRCNAKLNLTSRAL
DPAGNESAYPPNGVECYSCVGLSREACQGTSPPVSCYNASDHVYKGCFDGNVTILTAAANVTV
SLPVRCVQDEFCTRDTGVTGPGFTLSGS~~CC~~QGSRCNSDLRNKYFSPRIPLVRLPPPEPTT
VASTTSVTTSTSAPVRPTSTTKPMPAPTSQT~~PRQ~~GVEHEASRDEEPRLTGGAAGHQDRSNSG
QYP~~A~~KGGPQQPHNKGCVAPTAGLAALLAVAAGVLL

FIGURE 126

CGGGACTCGGCGGGCCTCCTGGGAGTCTCGGAGGGACCGGCATGAGT
 TGGTGTGGCTTCCTCTGCAGCCTGCTGGCCCCATGGCCTGCCAGTGCAGCTGAAAAG
 GAGAAGGAAATGGACCCCTTTCATTATGATTACAGACCCCTGAGGATTGGGGACTGGTGT
 CGCTGTGGCCTCTCGGTTGGATCCTCCTATCCTAAGTCGCAGGTGCAAGTGCAGTT
 TCAATCAGAACAGCCCCGGGCCCCAGGAGATGAGGAAGCCCAGGTGGAGAACCTCATCACCGCC
 AATGCAACAGAGCCCCAGAACGAGAACACTGAAGTGCAGCCATCAGGTGGAAGCCTCTGGAA
 CCTGAGGGCGCTGCTGAACCTTGGATGCAAATGTCGATGCT**TAA**GAAAACCGGCCACTTC
 AGCAACAGCCCTTCCCCAGGAGAACGCAAGAACCTGTGTGTCCCCCACCTATCCCTCTA
 ACACCATTCCACCTGATGATGCAACTAACACTTGCCCTCCCCACTGCAGCCTGCGGTCT
 GCCCACCTCCGTATGTGTGTGTGTGTACTGTGTGTGTTGCTAACTGTG
 GTCTTGTTGGCTACTTGTGTGGATGGTATTGTGTGTTAGTGAACGTGGACTCGCTT
 CCCAGGCAGGGGCTGAGCCACATGCCATCTGCTCCTGCCGTGGCCCTCCATCAC
 CTTCTGCTCCTAGGAGGCTGCTGTGCCCAGACCAGCCCCCTCCCTGATTAGGGATGC
 GTAGGGTAAGAGCACGGCAGTGGCTTCAGTCGTTGGACCTGGGAAGGTTGCAGCAC
 TTTGTATCATTCTCATGGACTCCTTCACCTTAACAAAAACCTGCTCCTTATCCC
 ACCTGATCCCAGTCTGAAGGTCTTAGCAACTGGAGATAAAAGCAAGGAGCTGGTGAGCC
 CAGCGTTGACGTCAAGGCAGGCTATGCCCTCCGTGTTAATTCTCCAGGGGCTTCCACG
 AGGAGTCCCCATCTGCCCGCCCTTCACAGAGCGCCGGGATTCCAGGCCAGGGCTTCT
 ACTCTGCCCTGGGAATGTGTCCCCTGCATATCTTCAGCAATAACTCCATGGCTCTGG
 GACCCTACCCCTCCAACCTCCCTGCTCTGAGACTCAATCTACAGCCCAGCTCATCCAG
 ATGCAGACTACAGTCCCTGCAATTGGGTCTGGCAGGCAATAGTTGAAGGACTCCTGTTCC
 GTTGGGCCAGCACACGGGATGGATGGAGGGAGAGCAGAGGCCCTTGCTCTGCCTACG
 TCCCCTAGATGGCAGCAGAGGCAACTCCGCATCCTTGCTCTGCCTGCGTGGTCAGA
 GCGGTGAGCGAGGTGGGTTGGAGACTCAGCAGGCTCCGTGAGGCCCTGGAACAGTGAGAG
 GTTGAAGGTATAACGAGAGTGGGAACTCACCCAGATCCCAGGCCCTCTGTCTGTGTT
 CCCCGGAAACCAACCAACCGTGCCTGTGACCCATTGCTGTTCTGTATCGTATCT
 CCTCAACACAACAGAAAAAGGAATAAAATCCTTGTTCCT

FIGURE 127

MELVLVFLCSLLAPMVLASAAEKEKEMDPFH^YQTLRIGGLVFAVVLFSVGILLILSRRCK
CSFNQKPRAPGDEEAQVENLITANATEPQKQRTEVQPSGGSLWNRLRLLEPLDANVDA

FIGURE 128

AAACTGACGCCATGAAGATCCC GGTCCTCCTGCCGTGGTGCTCCTCTCCCTCCTGGTGCT
CCACTCTGCCAGGGAGCCACCCTGGGTGGTCTGAGGAAGAAGCACCATTGAGAATTATG
CGTCACGACCCGAGGCCTTAACACCCCGTTCTGAACATCGACAAATTGCGATCTGCGTTT
AAGGCTGATGAGTCCTGAAC TGGCACGCCCTTTGAGTCTATCAAAGGAAACTCCTTT
CCTCAACTGGGATGCCTTCTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCAGT
G**A**CCATGACCTCCACTGGAAGAGGGGGCTAGCGTGAGCGCTGATTCTAACCTACCATAACT
CTTCCTGCCTCAGGAACTCCAATAAACATTTCCATCCAAA

FIGURE 129

MKIPVLPAVVLLSLLVLHSAQGATLGGPEEESTIENYASRPEAFNTPFLNIDKLRSAFKADE
FLNWHALFESIKRKLPFLNWDAFPKLKGLRSATPDAQ

FIGURE 130

CAGTTCTGAAATCAATGGAGTTAATTAGGAAATACAAACCAGCC**ATGGGGTGGAGATTGC**
CTTGCCCTCAGTGATTCTCACCTGCCTCTCCCTCTGGCAGCAGGAGTCTCCCAGGTTGTC
TTCTCCAGCCAGTCCAACTCAGGAGACAGGTCCAAGGCCATGGGAGATCTCTCCTGTGGC
TTTGC CGGCCACTCA**TGA**GAGTGTTTGTAAGTATTTAGAATACTGTTGACTTCT
TCATGATTTAATAACCACATCCTTGCGAAGTTATGAGGCTTAGGGGAATGTCAACCCCTCA
AATTTTGTTATACTAGATGGCTTCCATTACCCACCACTATTTAAGGTCCCTTATTTT
AGGTTCAAGGTTCATTGACTTGAGAAAGTGCCTCTGCAGCTTCATTGATTGTTTATC
TTCACTATTAATTGTAACGATTAAAAAGAATAAGAGCACGCAGACCTCTAGGAGAATATT
TATCCCTGGGTGCCCTGACACATTATGTAGTGATCCCACAAATGTGATTGTTAATTAAA
TGTTATTCTAATATTAGTACATTCAAGTTGATGTAATATGAATAACCAGAATCTATTCTT
AAAAGTTTGAGTATTTCAACTAGATATTGTATAGAAAGACTGAATAGTGATG

FIGURE 131

MGVEIAFASVILTCLSLLAAGVSQVVLLQPVPTQETGPKAMGDLSCGFAGHS

FIGURE 132

GGGGAATCTGCAGTAGGTCTGCCGGCG**ATG**GAGTGGTGGCTAGCTGCCGTTGGCTCTG
 GCTGCTGTTGTTCCCTGCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAAATGGA
 AAGTATTATTGACCAAATAACAGGTCTTGGAGAATTACGAACCATGTTCAAGTCAAAAC
 TGCAGCTGCTACCATGGTGTAGAGAAGAGGATCTAACCTCCGAGGAGGCATCTCCAG
 GAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCACTAAGAAC
 GACTGTACCAGGGAAAATGACTGCATGTTCCCCTCAAGGTGTAGTGGTGTGAGCACTTATT
 TTGGAAGTGATCGGGCGTCCCTGACATGGAGATGGTGTCAATGTACGAGATTATCCTCA
 GGTTCTAAATGGATGGAGCCTGCCATCCCAGTCTTCAGTAAGACATCAGAGTACC
 ATGATATCATGTATCCTGCTTGGACATTGGAGGGGACCTGCTGTTGGCCAATTAT
 CCTACAGGTCTTGGACGGTGGGACCTCTCAGAGAACATCTGGTAAGGTCAAGCACAGTG
 GCCATGGAAAAAGAAAAACTCTACAGCATATTCCGAGGATCAAGGACAAGTCCAGAACGAG
 ATCCTCTCATTCTCTGTCTCGGAAAACCCAAAATTGTTGATGCAGAATAACACCAAAAC
 CAGGCCTGGAAATCTATGAAAGATACTTAGGAAAGCCAGTGCTAAGGATGTCCATCTTGT
 GGATCACTGCAAATACAAGTATCTGTTAATTTCGAGGCGTAGCTGCAAGTTCCGGTTA
 AACACCTCTCCTGTGGCTCACTGTTTCCATGTTGGTGTAGTGAGTGGCTAGAATTCTC
 TATCCACAGCTGAAGCCATGGGTTCACTATATCCCAGTCAAAACAGATCTCTCCAATGTCCA
 AGAGCTGTTACAATTGTAAAAGCAAATGATGATGAGCTCAAGAGATTGCTGAAAGGGAA
 GCCAGTTATTAGGAACCATTGCAGATGGATGACATCACCTGTTACTGGAGAACCTCTTG
 AGTGAATACTCTAAATTCTGTCTTATAATGTAACGAGAAGGAAAGGTTATGATCAAATTAT
 TCCCAAAATGTTGAAAATGAACT**TAG**TAGTCATCATAGGACCATAGTCCTTTGTGGCA
 ACAGATCTCAGATATCCTACGGTGAGAAGCTTACCATAGCTGGCTCCTATACCTGAATA
 TCTGCTATCAAGCCAAATACCTGGTTTCCATTATGCTGCAACCTGTTACTGGAGAACCTCTTG
 AAGATTTAAAATGTGTCTAATACACTGATGATGAAGCAGTTCAACTTTGGATGAATAAGGA
 CCAGAAATCGTGAGATGTGGATTGGACCCAACTCTACCTTCACTGGTAAATTGACTGTCCA
 ACAGCTTGTGCCTCAGATCATCCACCTGTTGAGTCCATCACTGAAATTGACTGTCCA
 TGTGATGATGCCCTTGTCCCATTATTGGAGCAGAAAATTGTCATTGGAAAGTAGTACAA
 CTCATTGCTGGAATTGTGAAATTATTCAAGGCAGTGATCTCTGTCACTTATTAAATGTAGG
 AAACCCATTGGGTTATGAAAATACTTGGGGATCATTCTCTGAATGGTCTAAGGAAGCGG
 TAGCCATGCCATGCAATGATGTTAGGAGCTCTTTGTAAGGAAACTCTGTTACTCAG
 GAGGTTCTATAATGCCACATAGAAAGAGGCCATTGCATGAGTAATTATTGCAATTGGATT
 TCAGGTTCCCTTTGTGCCCTCATGCCCTACTTCTTAATGCCCTCTAAAGCCAAA

FIGURE 133

MEWWASSPLRLWLLLFLPSAQGRQKESGSWKVFIDQINRSLENYPECSSQNCSCYHGVIE
EDLTPFRGGISRKMMAEVVRRKLGTHYQITKNRLYRENDCMFPSRCSGVEHFILEVIGRLPD
MEMVINVRDYPQVPKWMEPAIPVFSFSKTSEYHDIMYPAWTFWEGGPAVWPIYPTGLGRWDL
FREDLVRSAAQWPWKKKNSTAYFRGSRTSPERDPLILLSRKNPKLVDAEYTKNQAWKSMKDT
LGKPAAKDVHLVDHCKYKYLNFNFRGVAASFRFKHLFLCGSLVFHVGDEWLEFFYPQLKPWVH
YIPVKTDLSNVQELLQFVKANDDVAQEIAERGSQFIRNHLQMDDITCYWENLLSEYSKFLSY
NVTRRKGYDQIIPKMLKTEL

FIGURE 134

CACCCCTCCATTCTGCCATGGCCCTGCACTGCTCCTGATCCCTGCTGCCCTGCCTCTT
 TCATCCTGGCCTTGGCACCGGAGTGGAGTTCGTGCCTTACCTCCCTCGGCCACTTCTT
 GGAGGGATCCCGGAGTCTGGTGGTCCGGATGCCGCCAGGGATGGCTGGCTGCCCTGCAGGA
 CCGCAGCATCCTGCCCTGGCATGGATCTGGGCTCCTGCTTCTATTGTTGGGCAGC
 ACAGCCTCATGGCAGCTGAAAGAGTGAAGGCATGGACATCCCAGTACTTGGGTCCTCAG
 AGGTCACTGTATGTGGCCTGCACTGCCCTGGCCTGCAGCTGGTATGCGGTACTGGGAGCC
 CATAACCAAAGGCCCTGTGTTGGGAGGCTGGGCTGAGCCATGGCCACCTGGGTGCCGC
 TCCTCTGCTTGCTCCATGTCATCTCCTGGCTCCTCATCTTAGCATCCTCTCGTCTTT
 GACTATGCTGAGCTCATGGCCTCAAACAGGTATACTACCATGTGCTGGGCTGGCGAGCC
 TCTGGCCTGAAGTCTCCCCGGCTCTCAGACTCTCTCCACCTGCCACCCAGTGTGTG
 TGGAGCTGCTGACAGTGTGGTGGTGCCTACCTGGCACGGACCGTCTCCTTGCT
 TTCCTCCTACCCCTCACCTGGCCTGGCTCACGGCTTGATCAGCAAGACCTCCGCTACCT
 CGGGCCCAGCTACAAAGAAAACCCACCTGCTCTCGGCCAGGATGGGAGGCAGAGT
GAGGAGCTCACTCTGGTTACAAGCCCTGTTCTCCTCTCCACTGAATTCTAAATCCTAAC
 ATCCAGGCCCTGGCTGTTCATGCCAGAGGCCAAATCCATGGACTGAAGGAGATGCCCTT
 CTACTACTTGAGACTTATTCTCTGGTCCAGCTCCATACCCTAAATTCTGAGTTCAGCCA
 CTGAACCTCCAAGGTCCACTCTCACCAAGCAAGGAAGAGTGGGTATGGAAGTCATCTGCC
 TTCACTGTTAGAGCATGACACTCTCCCCCTCAACAGCCTCTGAGAAGGAAAGGATCTGCC
 CTGACCACTCCCCGGACTGTTACTGCCTCTGCCTCAGGGTCCCTCTGCCACCGCT
 GGCTTCCACTCCAAGAAGGTGGACCAGGGCTGCAAGTTAACGGTCATAGCTGCCCTCCA
 GGCCCCAACCTGCCTCACCACTCCGGCCCTAGTCTGACCTCCTAGGCCCTGCCCT
 GGGCTCAGACCCCAACCTAGTCAAGGGGATTCTCCTGCTCTAACCGATGACTGGGCTC
 CCTGCTCTCCGAGGAAGATGCTCTGCAGGAAAATAAAAGTCAGCCTTTCTAAAAAAA

FIGURE 135

MAPALLIIPAALASFILAFGTGVEFVRFTSLRPLLGGIPESGGPDARQGWLAALQDRSILAP
LAWDLGLLLLFGQHSLMAAERVKAWTSRYFGVLQRSLYVACTALALQLVMRYWEPIPKGPV
LWEARAEPWATWVPLLCFVLHVVISWLLIFSILLVFDYAELEMGLKQVYYHVLGLGEPLALKSP
RALRLFSHLRHPVCVELLTVLWVVPTLGDRLLAFLLTLYLGLAHGLDQQDLRYLRAQLQR
KLHLLSRPQDGAE

Signal sequence:

amino acids 1-13

Transmembrane domains:

amino acids 58-76, 99-113, 141-159, 203-222

N-myristoylation sites:

amino acids 37-43, 42-48, 229-235

FIGURE 136

CCGAGCACAGGAGATTGCCTGCGTTAGGAGGTGGCTGC GTGGAAAAGCTATCAAGGA
 AGAAATTGCCAACCATGTCTTTCTGTTTCAGAGTAGTCACAAACAGATCTGAGTGT
 TTAATTAAGCATGGAATACAGAAAACAACAAAAACTTAAGCTTAATTCTATCTGGAATT
 CCACAGTTCTTAGCTCCCTGGACCCGGTTGACCTGTTGGCTCTCCCGCTGGCTGCTCTA
 TCACGTGGTGCCTCCGACTACTCACCCCCGAGTGTAAGAACCTTCGGCTCGCGTGCCTCTG
 AGCTGCTGTGG**ATG**GCCTCGGCTCTGGACTGTCCTCCGAGTAGGATGTCACTGAGATCC
 CTCAAATGGAGCCTCGTGTGTCACTCCTGAGTTCTTGATGTGGTACCTCAGCCT
 TCCCCACTACAATGTGATAGAACGCGTGAACGGATGACTTCTATGAGTATGAGCCGATT
 ACAGACAAGACTTCACTCACACTCGAGAGCATTCAAAC TGCTCTCATCAAATCCATT
 CTGGTCATTCTGGTGACCTCCCACCCTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTAC
 TTGGGGTGAAGAAAGTCTGGTGGGATATGAGGTTCTTACATTTCTTATTAGGCCAAG
 AGGCTGAAAAGGAAGACAAAATGTTGGCATTGTCCTAGAGGATGAACACCTTCTTATGGT
 GACATAATCCGACAAGATTTTAGACACATATAAACCTGACCTGAAAACCATTATGGC
 ATTCAAGGTGGTAACTGAGTTGCCAATGCCAAGTACGTAATGAAGACAGACACTGATG
 TTTCATCAAACTGGCAATTAGTGAAGTATCTTAAACCTAAACCACACTCAGAGAAGTT
 TTCACAGGTTATCCTCTAATTGATAATTATTCCCTATAGAGGATTTACCAAAAAACCCATAT
 TTCTTACCAAGGAGTATCCTTCAAGGTGTTCCCTCCACTGCAGTGGTTGGTTATATAA
 TGTCCAGAGATTTGGTGCCAAGGATCTATGAAATGATGGTCACGTAAAACCCATCAAGTT
 GAAGATGTTATGTCGGATCTGTTGAATTATTAAAAGTGAACATTCAATTCCAGAAGA
 CACAAATCTTCTTCTATAGAATCCATTGGATGTCTGTAACGTGAGACGTGATTG
 CAGCCCATGGCTTTCTCCAAGGAGATCATCACTTTGGCAGGTATGCTAAGGAACACC
 ACATGCCATTAT**TAA**CTTCACATTCTACAAAAGCCTAGAAGGACAGGACACCTGTGGAAA
 GTGTTAAATAAAAGTAGGTACTGTGGAAAATTCACTGGGAGGTCACTGTGCTGGCTTACACTG
 AACTGAAACTCATGAAAACCCAGACTGGAGACTGGAGGGTTACACTGTGATTATTAGTC
 AGGCCCTCAAAGATGATATGTGGAGGAATTAAATATAAGGAATTGGAGGTTTGCTAA
 GAAATTAAATAGGACCAACAATTGGACATGTCATTCTGTAGACTAGAATTCTAAAAGGG
 TGTTACTGAGTTATAAGCTCACTAGGCTGAAAAACAAAATGTAGAGTTATTG
 AACAAATGTAGTCACTGAGGTTGTATCTTATGTGGATTACCAATTAAAATATA
 TGTAGTTCTGTGTCAAAACCTCTCACTGAAGTTACTGAACAAAATTACCTGTTT
 TGGTCATTATAAAAGTACTTCAAGATGTTGCAGTATTCACAGTTATTATTAAAATTA
 CTTCAACTTGTGTTTAAATGTTGACGATTCAATACAAGATAAAAAGGATAGTGAAT
 CATTCTTACATGCAAACATTCCAGTTACTTAACGTGATCAGTTATTATTGATACATCAC
 TCCATTAATGTAAGTCATAGGTATTGCATATCAGTAATCTGGACTTGTAAAT
 ATTTACTGTGGTAATAGAGAAGAATTAAAGCAAGAAAATCTGAAAA

FIGURE 137

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPIYRQDFHFTLREHSNC SHQNPFLVILVTSHPSDV KARQAIRVTWGEKKSSWWGYEVLTFFLLGQEAEKEDKMLALSLEDEHLLY GDIIRQDFLDTYNNLTLKTIMAFRWTEFCPNAKYVMKTDTDVFINTGNLVKYILLNLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQEYPFKVFPPYCSGLGYIMSRLVPRIYEMMGHVKPIKFEDVYVGICLNLLKVNIHIPEDTNLFFLYRIHLDVCQLRRVIAAHGFSSKEIITFWQVMLRNTTCHY

FIGURE 138

CCTCTGTCCACTGCTTCGTGAAGACAAGATGAAGTTACAATTGTCTTGCTGGACTTCTT
GGAGTCTTCTAGCTCCTGCCCTAGCTAACTATAATCAACGTCAATGATGACAACAACAA
TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAATGAACACAATGTGGCCAATGTTGACA
ATAACAACGGATGGGACTCCTGGAATTCCATCTGGGATTATGGAAATGGCTTGCTGCAACC
AGACTCTTCAAAAGAACATGCATTGTGCACAAAATGAACAAGGAAGTCATGCCCTCCAT
TCAATCCCTTGATGCACTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC
CTCCCCAAGGGCCTGATGTACTCAGTCACCCAAACAAAGTCGATGACCTGAGCAAGTCGGA
AAAAACATTGCAAACATGTGCGTGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC
AAGCCTGTTTTTACTCAGGAACGTGCTACACGACCAGTGTACTATGGATTGTGGACATT
CCTTCTGTGGAGACACGGTGGAGAACTAAACAATTAAAGCCACTATGGATTAGTCAT
CTGAATATGCTGTGCAGAAAAAATGGGCTCCAGTGGTTTACCATGTCATTCTGAAATT
TTTCTCTACTAGTTATGTTGATTCTTAAGTTCAATAAAATCATTAGCATTGAAAAAAA

FIGURE 139

MKFTIVFAGLLGVFLAPALANYNINVNDNNNAGSGQQSVVNNEHNVANVDNNNGWDSWNS
IWDYGNNGFAATRLFQKKTCIVHKMNKEVMPSIQSLDALVKEKKLQGKGPGGPPPGLMYSVN
PNKVDDLSKFGKNIANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCGDTVEN

Signal Peptide:

amino acids 1-20

N-myristoylation Sites:

amino acids 67-72, 118-123, 163-168

Flavodoxin protein homology:

amino acids 156-174

FIGURE 140

CATTCTGAAACTAACGTGTCAGAATTGACTTGAAAAGCATTGCTTTACAGAAGTATA
 TTAACCTTTAGGAGTAATTCTAGTTGGATTGTAATATGAAATAATTAAAAGGGCTTCG
 CTCATATATAGGAAAATCGCATATGGCCTAGTATTAAATTCTATTGCTTACTGATTTTT
 TGAGTTAAGAGTTGTTATATGCTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAA
 GAATAAAGTAGATTGAGTCTCCAATTATGTAAGCTCAGAAGAACTGGTTGTTACATG
 CAAGCTTATAGTTGAAATATTTCAAGGAATTACATGAATGACAGTCTCGAACCAATGTGT
 TTGTTCGATTCAACCAGAGACTATAGCATGTGCTGCATCTACCTTGAGCTAGAGCACTT
 CAGATTCCGTTGCCAACTCGTCCCCATTGGTTCTCTTTGGTACTACAGAAGAGGAAAT
 CCAGGAAATCTGCATAGAAACACTTAGGTTATACCAGAAAAAGCCAAACTATGAATTAC
 TGGAAAAAGAAGTAGAAAAAGAAAAGTAGCCTACAAGAAGCCAAATTAAAAGCAAAGGGA
 TTGAATCCGGATGGAACTCCAGCCCTTCAACCCTGGGTGGATTTCTCCAGCCTCCAAGCC
 ATCATCACCAAGAGAAGTAAAGCTGAAGAGAAATCACCAATCTCCATTAATGTGAAGACAG
 TCAAAAAAGAACCTGAGGATAGACAACAGGCTCCAAAGCCCTACAATGGTGTAAAGAAAA
 GACAGCAAGAGAAGTAGAAATAGCAGAAGTGCAGTCGATCGAGGTCAAGAACACGATCACG
 TTCTAGATCACATACTCCAAGAAGACACTATAATAATAGGCGGAGTCGATCTGGAACATACA
 GCTCGAGATCAAGAAGCAGGTCCCGCAGTCACAGTGAAAGCCCTCGAAGACATCATAATCAT
 GGTTCTCCTCACCTTAAGGCCAAGCATACCAAGAGATGATTAAAAAGTCAAAACAGACATGG
 TCATAAAAGGAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAG
 CCAAGAAACACAGGCATGAAAGGGACATCATAGGGACAGGCGTGAACGATCTCGCTCCTT
 GAGAGGTCCCATAAAAGCAAGCACCAGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCG
CTGACTTCTCTTCTTGAGCCTGCATCAGTTCTGGTTGCCTATCTACAGTGTGATGT
 ATGGACTCAATCAAAACATTAAACGCAAACGTGATTAGGATTGATTCTGAAACCCCTCTA
 GGTCTCTAGAACACTGAGGACAGTTCTTGAAAAGAACTATGTTAATTGGCACATT
 AAAATGCCCTAGCAGTATCTAATTAAAAACCATGGTCAGGTTCAATTGTACTTTATTATAGT
 TGTGTATTGTTATTGCTATAAGAACTGGAGCGTGAATTCTGAAAAATGTATCTTATT
 ATACAGATAAAATTGAGACACTGTTCTATTAAAGTGGTTATTGTTAAATGATGGTGAAT
 ACTTTCTTAACACTGGTTGTCATGTGTAAAGATTACAGGAAATAAAACAAAT
 CTTGTTTTCTAAAAAAAAAAAAAGT

FIGURE 141

MNDSLRTNVFVRFQPETIACACIYLAARALQIPLPTRPHWFLLFGTTEEEIQEICIETLRLY
TRKKPNYELLEKEVEKRKVALQEAKLKAKGLNPDGTPALSTLGGFPASKPSSPREVKAEEK
SPISINVKTVKKEPEDRQQASKSPYNGVRKDSKRSRNSRSASRSRSRTRSRSRSHTPRRHYN
NRRSRSGTYSSRSRSRSRSHSESPRRHGNHGSPLKAKHTRDDLKSSNRHGHKRKKSRSRSQ
SKSRDHSDAAKKHRHERGHHDRRERSRSFERSHKSKHHGGSRSGHGRHRR

FIGURE 142

TGGGGATAAAGGAAAAATGGTCAGGTATTAATGGCTTAAAGATTATTGGAAGGGGTTATCA
TTTTTGAAANNNTATCGGGTCANAATTGNCTTGAAAAGCATTGCTTTACAGAAATATAT
TANCTTTAGAGTAATTCTAGTTGGATTGTAATATGAAATTATTAAAAGGGCTTCGCT
CATATATAGGAAAATCGCATATGGCCTAGTATTAAATTNTTATTGCTTACTGATTTTTG
AGTTAAGAGTTGTTATATGNTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAAGA
ATAAAAGTAGATTGAGTCTCCAATTATGTAAGCTTCAGAAGAACTGGTTGTTACATGCA
AGCTTATAGTTGAAATATTTCAAGGAATTACATGAATGACAGTCTCGAACCAATGTGTTT
GTTCGATTCAACCAGAGANTATAGCATGTGCTGCATCTACCTTGCAGNTAGAGCACTTCA
GATTCCGTTGCCAACTNGTCCCCATTGGTTCTTCTTTGGTACTACAGAAGAGGAAATCC
AGGAAATNTGCATAGAAACACTTAGGCTTATACCAGAAAAAGCCAAACTATGAATTACTG
GAAAAAGAAGTAGAAAAAGAAAAGTAGCCTACAAGAAGCCNAATTAAAAGCAAAGGGATT
GAATCCGGATGGAACTCCAGCCCTTCAACCCTGGGTGGATTTCTCC

FIGURE 143

GGCACGAGGCCTCGTCCAAGCTTGGCACGAGGGTGACCGCGTTCTCGCACCGC**ATGGC**
 GGTCCCTCGGAGTACAGCTGGTGGTACCCCTGCTCACTGCCACCCTCATGCACAGGCTGGCGC
 CACACTGCTCCTCGCGCCTGGCTGCTCTGTAACGGCAGTTGTTCCGATAACAAGCACCCG
 TCTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCCAGAGGCAGGAAAGAGCGGTG
 GGCCAAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCGAGATGCCCGTTCCAGCTGG
 AGACCTGCCCTCACGACCGTGGATGCCCTGGTCTCGCCTTCCCTGGAGTACCAAGTGG
 TTTGTGGACTTGCTGTACTCGGGCGCGTGTACCTCTTACAGAGGCCTACTACTACAT
 GCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGTGCCTGCTCACGGTGACCTCT
 CCATCAAGATGTTCTGACAGTGACACGGCTGTACTTCAGCGCCGAGGAGGGGGTGAGCGC
 TCTGTCTGCCTCACCTTGCCCTTCCCTGCTGCTGGCCATGCTGGTCAAGTGGTGC
 GGAGGAGACCCTCGAGCTGGCCTGGAGCCTGGCTGGCCAGCATGACCCAGAACTTAGAGC
 CACTTCTGAAGAAGCAGGGCTGGGACTGGCGCTTCTGTGGCCAAGCTGGCTATCCGCGT
 GGACTGGCAGTGGTGGGCTCTGTGCTGGTGCCTCACCCTCCCAGGCCTGCGGCTGGC
 CCAGACCCACCGGGACGCACTGACCATGTCGGAGGACAGACCCATGCTGCAGTTCCCTGC
 ACACCAAGCTTCTGTCTCCCTGTTCACTCTGTGGCTCTGGACAAAGCCATTGCACGGGAC
 TTCTGCACCAGCCGCCCTGGTGGTGGTGGCTGTGCCTGCTGCGGCTGGCGGTGACCCGGCCCC
 ACCTGCAGGCCTACCTGTGCCTGGCCAAGGCCGGTGGAGCAGCTGCGAAGGGAGGCTGGC
 CGCATCGAAGCCCGTGAAATCCAGCAGAGGGTGGTCCGAGTCTACTGCTATGTGACCGTGGT
 GAGCTTGCAGTACCTGACGCCGCTCATCCTCACCCCTCAACTGCACACTTCTGCTCAAGACGC
 TGGGAGGCTATTCCCTGGGCCCTGGGCCAGCTCCTCTACTATCCCCGACCCATCCTCAGCC
 AGCGCTGCCCATCGGCTCTGGGAGGACGAAGTCCAGCAGACTGCAGCGGGATTGCCGG
 GGCCCTGGTGGCCTGCTTACTCCCTCTTCCGTGGCGTCTGGCCTACCTCATCTGGT
 GGACGGCTGCCAGCTGCTGCCAGCCTTCCGTGGCGTCTACTTCCACCAAGCAGTGGCA
 GGCTCC**TAG**CTGCCTGCAGACCCCTCTGGGCCCTGAGGTCTGTTCTGGGCCAGCGGGACA
 CTAGCCTGCCCTCTGTTGCGCCCCGTGTCCCCAGCTGCAAGGTGGGCCGGACTCCCC
 GGCGTTCCCTCACCAAGTGCCTGACCCGCCCTGGACGCCAGTTCTGCCTCA
 GAACTGTCTCCCTGGGCCAGCAGCATGAGGGTCCCGAGGCCATTGTCTCCGAAGCGTATG
 TGCCAGGTTGAGTGGCGAGGGTGATGCTGGCTGCTCTGAACAAATAAAGGAGCATGCC
 GATTTTAA

FIGURE 144

MAVLGVQLVVTLTATLMHRLAPHCSFARWLLCNGSLFRYKHPSEEELRALAGKPRPRGRKE
RWANGLSEEKPLSVPRDAPFQLETCPLETVDALVLRFFLEYQWFVDFAVYSGGVYLFTTEAYY
YMLGPAKETNIAVFWCLLTVTFSIKMFLTVTRLYFSAEEGGERSVCLTFAFLFLLAMLVQV
VREETLELGLEPGLASMTQNLEPLLKKQGWDWALPVAKLAIRVGLAVVGSVLGAFLTFPGLR
LAQTHRDALTMSEDRPMLQFLLHTSFLSPLFILWLWTKPIARDFLHQPPFGETRFSLLSDSA
FDSGRLWLLVVLCLLRLAVTRPHLQAYLCLAKARVEQLRREAGRIEAREIQQRVVRVYCYVT
VVSLQYLTPILTLNCTLLKTLGGYSWGLGPAPLLSPDPSSASAAPIGSGEDEVQQTAARI
AGALGGILLTPLFLRGVLAYLIWWTAACQLLASLFGLYFHQHLAGS

FIGURE 145

CGTTNGCACGCGTCAATGGCGGTCTCGGAGTACAGCTGGTGGTACCCCTGCTCACTGCCAC
CCTCATGCACAGGCTGGCGCCACACTGCTCCTCGCGCCTGGCTGCTCTGTAACGGCAGTT
TGTTCCGATAACAAGCACCCGTNTTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCC
CAGAGGCAGGAAAGAGCGGTGGCCAATGCCCTAGTGAGGAGAAGCCACTGTCTGTGCC
GAGATGCCCGTCCAGCTGGAGACCTGCCCTCACGACCGTGGATGCCCTGGCCTGC
TTCTTCCTGGAGTACCAGTGGTTGTGGACTTGCTGTACTCGGGCGCGTGTACCTCTT
CACAGAGGCCTACTACTACATGCTGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGT
GCCCTGCTCACAGTGACCTCTCCATCAAGATGTTCTGACAGTGACACGGCTGTACTTCAGC
GCCGAGGAGGGGGGTGAGCGCTCTGTCTGCCTCACCTTGCCTTCCTGCTGCTGGC
CATGCTGGTGCAAGCG

FIGURE 146

GGTTCCATACCTCATCTGAGAATCAGAGAGCATAATCTTACGGGCCGTGATTTAAACGTGGCTT
 AATCTGAAGGTTCTCAGTCATAATTCTTGATCTACTGATTGTGGGGCATGGCAAGGTTGCTTAAGGAGC
 TTGGCTGGTTGGGCCCTGTAGCTGACAGAAGGTGGCAGGGAGAATGCAGCACACTGCTCGGAGA**ATGAAGG**
 CGCTTCTGTGCTGGCTTGCTGCTAAGTACAATGACAATGTGGCAACCTGCACTTCTG
 TATTAGAAGACTCTGAAAGGTGCTCCCACAGGCCCTGACCAAAGAGATAGGAAGAGGCCCTCACAAGATGGCTG
 TCCAGACGGCTGTGCGAGCCTCACAGGCCACGGCTCCCTCCCCAGAGGTTCTGCAGCTGCCACCATCTCCTTAA
 TGACAGACGAGCCTGGCTAGACAACCCTGCTACGTGCTCTGGCAGAGGACGGGAGCAATCAGCCCA
 GTGGACTCTGGCCGGAGCAACCGAACTAGGGCACGGCCCTTGAGAGATCCACTATTAGAAGCAGATCATTAA
 AAAAATAAATCGAGCTTGATGTTCTCGAAGGACAAAGAGCGGAGTCAGTTGCCAACCATGCCGACCAGG
 GCAGGGAAAATTCTGAAAACACCACTGCCCTGAAGTCTTCCAAGGTTGATACCACCTGATTCCAGATGGTGA
 ATTACCAAGCATCAAGATCAATCGAGTAGATCCCAGTGAAGGCTCTATATTAGCTGGTGGAGGTAGC
 CCCACTGGTCCATATCATTATCACAACATTATCGTATGGGGTGAATGCCAGAGACGGCCGGCTACTGCCAG
 GAGACATCATTCTAAAGGTCAACGGATGGACATCAGCAATGCTCTCACAACTACGCTGTGCGTCTCTGCC
 CAGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTAACAGAAGTCCGCAGCAGGAACAATGGACAGGCC
 GGATGCCTACAGACCCGAGATGACAGCTTCATGTGATTCTCAACAAAGTAGCCCCGAGGAGCAGCTGGAA
 TAAAACGGTGCAGCAAGGTGGATGAGCCTGGGTTTCATCTCAATGTGCTGGATGGCGTGTGGCATATCGA
 CATGGTCAGCTTGAGGAGAATGACCGTGTGTTAGCCATCAATGGACATGATCTCGATATGGCAGCCCAGAAAG
 TGGCGCTCATCTGATTCAGGCCAGTGAAGACGTGTTCACCTCGTGTCCGCCAGGTTGGCAGCGGAGCC
 CTGACATCTTCAGGAAGCCGGCTGGAACAGCAATGGCAGCTGGTCCCCCAGGGCAGGGGAGAGGAGCAACACT
 CCAAGCCCCCTCCATCCTACAATTACTGTGATGAGAAGGTGGTAAATATCCAAAAGACCCGGTGAATCTCT
 CGGCATGACCGTCGCAGGGGGAGCATCACATAGAGAATGGGATTGCTATCTATGTGATCAGTGTGAGCC
 GAGGAGTCATAAGCAGAGATGGAAGAATAAAAACAGGTGACATTGTTGAATGTGGATGGGTCGA
 GAGGTCAGCCGGAGTGGCAGTGGCATTATTGAAAAGAACATCATCTCGATAGTACTCAAAGCTTGGAAAGT
 CAAAGAGTATGAGCCCCAGGAAGACTGCAGCAGCCCAGCAGCCCTGGACTCCAACCACATGGCCCCACCCA
 GTGACTGGTCCCCATCTGGGTATGTGGCTGGATTACACGGTGTGTATAACTGTAAAGATATTGTATT
 CGAAGAAACACAGCTGAAAGTCTGGCTTCTGCATTGTTAGGAGGTATGAAGAATACAATGGAAACAAACCTT
 TTTCATCAAATCCATTGTTGAAGGAACACCAAGCATACAATGATGGAAGAATTAGATGTGGTGA
 CTGTCATGGTAGAAGTACATCAGGAATGATACATGCTTGGCTGGCAAGACTGCTGAAAGAAACTAAAGGAAGA
 ATTACTCTAACTATTGTTCTTGGCCTGGACTTTTA**TAGA**ATCAATGATGGGTCA
 GAGGAAACAGAAACTATTTATTTTATTTAAAGAAAGAATACATTGT
 TCACAAATAGGCTAAGAAGTGAACACTATTTATTTTATTTAAAGAAAGAATACATTGT
 AAAAATGTCAAGGAAAAGTATGATCATCTAAATGAAAGCAGTTACACCTCAGAAAATATGATTCCA
 AAAACTACTGTTCTCAGTGTGGAGGATTCTCATTACTCTACAACATTGTTATTTTCTATTCAAT
 AAAAGCCCTAAACAACTAAATGATTGATTGTATACCCCAGTGAATTCAAGCTGATTAAATTAAATT
 GGTATATGCTGAAGTCTGCCAAGGGTACATTATGCCATTAAATTACAGCTAAATATTAAATT
 TTGCTGAGAACGTTGCTTCATCAAACAGAATAATTTCAGAAGTTAAA

FIGURE 147

MKALLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPDGCA
SLTATAPSPEVSAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDGSRSNRARP
FERSTIRSRFFKKINRALSVLRRTKSGAVANHADQGRENSENTTAPEVFPRLYHLIP
DGEITSIKINRVDPSESLSIRLVGGSETPLVHIIIQHIYRDGVIARDGRLLPGDIIL
KVNGMDISNVPHNYAVRLLRQPCQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSF
HVILNKSSPEEQLGIKLVRKVDEPGVFIFNVLDGGVAYRHGQLEENDRVL
AINGHDLRYGSPEAAHLIQASERRVHLVVSQRQVQRSPDIFQEAGWNSNG
SWSPGPERSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVAGGASHRE
WDLPIYVISVEPGGVISRDGRIKTGDILLNVDGVELTEVRSEAVALLKRT
SSSIVLKALEVKEYEPQEDCSSPAALDSNHNMAPPDWSPSWVMWLELPRCL
YNCKDIVLRRNTAGSLGFCIVGGYEEYNGNKPFFIKSIVEGT
PAYNDGRIRCGDILLAVNGRSTSGMIHAACLARLLKELKGRI
TLTIVSWPGTFL

FIGURE 148

CCAAAGTGATCATTGAAAAAGAGATATCCACATCTTCAAGCCATATAAAGGATAGAAGCT
GCACAGGGCAGCTTACTTACTCCAGCACCTCCTCTCCCAGGCCA**ATG**GTCGACCATCT
TTGGGATACAATCTCATGGATAACGAGGTTTAACATCATCAGCCCCAAGCAACAATGGTGGC
AATGTTCAGGAGACAGTGACAATTGATAATGAAAAAAATACCGCCATCGTTAACATCCATGC
AGGATCATGCTCTTACCAACATTTGACTATAAACATGGCTACATTGCATCCAGGGTGC
TCTCCCGAAGAGCCTGCTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAAT
CTCCAATGGTACATCTATGAGAACACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTG
GGTCAAGTACAACCCCTCTGGAGTCTGTGATCAAAGACGTGGATTGGTCCTGCTGGTCAC
CCATTGAGAAACTCTGCAAACATATCCCTTGATAAGGGGGAGTGGTGAAAACACACAT
AATGTCGGTGCTGGAGGCTGTGCAAAGGCTGGCTCCGGCATCTGGGAATTCAATCTG
TGCAGACATTGTT**TAG**GATGATTAGCCCTTGTTATCTTCAAAGAAATACATCC
TTGGTTTACACTCAAAAGTCAAATTAAATTCTTCCAAATGCCCAACTAATTGAGATTC
AGTCAGAAAATATAATGCTGTATTATA

FIGURE 149

MKILVAFLVVLTIFGIQSHGYEVFNIISPSNNGGNVQETVTIDNEKNTAIVNIHAGSCSSTT
IFDYKHGYIASRVLSRRACFILKMDHQNIPLNNLQWYIYEKQALDNMFSNKYTWKYNPLE
SLIKDWDWFLLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV

FIGURE 150

GGCACGAGCCAGGAACTAGGAGGTTCTCACTGCCCGAGCAGAGGCCCTACACCCACCGAGGC
ATGGGGCTCCCTGGCTGTTCTGCTTGGCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCACG
GGAGGAAGAAATTACCCCTGTGGTCTCCATTGCCTACAAAGTCCTGGAAGTTTCCCCAAAG
GCCGCTGGGTGCTCATAACCTGCTGTGCACCCCAGCCACCACGCCATCACCTATTCCCTC
TGTGGAACCAAGAACATCAAGGTGCCAAGAAGGTGGTGAAGACCCACGAGCCGGCCTCCTT
CAACCTCAACGTACACTCAAGTCCAGTCCAGACCTGCTCACCTACTTCTGCCGGCGTCCT
CCACCTCAGGTGCCCATGTGGACAGTGCCAGGCTACAGATGCACTGGGAGCTGTGGTCCAAG
CCAGTGTCTGAGCTGCCGGCCAACTCACACTGCAGGACAGAGGGCAGGCCAGGGTGG
GATGATCTGCCAGGCCTCGGGCAGCCCACCTATCACCAACAGCCTGATGGGAAGGATG
GGCAGGTCCACCTGCAGCAGAGACCATGCCACAGGCAGCCTGCCAATTCTCCTGCC
AGCCAGACATCGGACTGGTCTGGTGCAGGCTGCAAACAACGCCAATGTCCAGCACAGCG
CCTCACAGTGGTCCCCCAGGTGGTGAACAGAAGATGGAGGACTGGCAGGGTCCCCTGGAGA
GCCCATCCTGCCCTGCCGCTCTACAGGAGCACCCGCCGTCTGAGTGAAGAGGGAGTTGGG
GGGTTCAAGGATAGGAATGGGAGGTCAAGGACGCAAAGCAGCAGGCCATG**TAGA**ATGAACC
GTCCAGAGAGCCAAGCACGGCAGAGGACTGCAGGCCATCAGCGTGCAGTGTGTTGG
GTTCATGCAAAATGAGTGTGTTAGCTGCTTGCACAAAAAAAAAAAAAAA

FIGURE 151

MGLPGLFCLAVLAASSFSKAREEEITPVVSIAYKVLEVFPKGRWVLITCCAPQPPPITYSL
CGTKNIKVAKKVVVKTHEPASFNLNVTLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK
PVSELRANFTLQDRGAGPRVEMICQASSGSPPITNSLIGKDGVHLQQRPCHRQPANFSFLP
SQTSDFWCQAANNANVQHSALTVVPPGGDQKMEDWQGPLESPILALPLYRSTRRLSEEEFG
GFRIGNGEVRGRKAAAM

Signal Peptide:

amino acids 1-18

N-glycosylation Sites:

amino acids 86-89, 132-135, 181-184

FIGURE 152

GGTCCTTAATGGCAGCAGCCGCCGCTACCAAGATCCTCTGTGCCCTCCGCTTGTCTCG
CTGTCCGGCTGGTCCCAGGGCTGGCGAGCCGACCCTCACTCTCTTGCTATGACATCACCGT
CATCCCTAAAGTTCAGACCTGGACCACGGTGGTGTGCCGTTCAAGGCCAGGTGGATGAAAAGA
CTTTTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCAGTCCCCTGGGGAAAGAAA
CTAAATGTCACAACGGCCTGGAAAGCACAGAACCCAGTACTGAGAGAGGGTGGACATACT
TACAGAGCAACTGCGTGACATTCACTGGAGAATTACACACCCAAGGAACCCCTCACCTGC
AGGCAAGGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTGGCAGTCAGT
TTCGATGGGCAGATCTTCCTCCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCC
TGGAGCCAGAAAGATGAAAGAAAAGTGGAGAATGACAAGGTTGTGGCCATGTCCTTCCATT
ACTTCTCAATGGGAGACTGTATAGGATGGCTTGAGGACTTCTGATGGCATGGACAGCACC
CTGGAGCCAAGTGCAGGAGCACCACCGCCATGTCCTCAGGCACAACCCAACTCAGGGCCAC
AGCCACCACCCCTCATCCTTGCTGCCCTCATCATCCTCCCCGCTTCATCCTCCCTGGCA
TCTGAGGAGAGTCCTTAGAGTGACAGGTTAAAGCTGATAACAAAAGGCTCTGTGAGCACG
GTCTTGATCAAACCTGCCCTCTGTCTGGCCAGCTGCCACGACCTACGGTGTATGTCCAGT
GGCCTCCAGCAGATCATGATGACATCATGGACCCAATAGCTCATTCACTGCCCTGATTCTT
TTGCCAACAAATTACCGAGCTTACACATATTATGCAATTCTCTTGCTGCTACC
TGATGGAATTCTGCACTTAAAGTTCTGGCTGACTAAACAAGATATATCATTCTTCTTC
TCTTTTGGAAATCAAGTACTTCTTGATGATCTCTTCTGCAAATGATATT
GTCAGTAAAATAATCACGTTAGACTCAGACCTCTGGGGATTCTTCCGTGAAAGAG
AATTTTAAATTATTAATAAGAAAAAATTATTAATGATTGTTCTTAGTAATTAT
TGTTCTGTACTGATATTAAATAAGAGTTCTATTCCAAAAA

FIGURE 153

MAAAAATKILLCLPLLLLSGWSRAGRAPHSLCYDITVIPKFRPGPRWCAVQGQVDEKTF
HYDCGNKTVPVSPLGKKLNVTAWKAQNPNLREVVDILTEQLRDIQLENYTPKEPLTLQAR
MSCEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFYFS
MGDCIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLLCCLLIILPCFILPGI

Important features:

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81

FIGURE 154

GGGAAAGCCATTCGAAAACCCATCTATAACAAACTATATTTCATTTCTGCTGCTAGCTG
CCTTGGGCCTCACAAATTCATTCTGTTCTGACTTCAGTATATAACCGTGG**ATGG**GAG
TTGATCCCAACCATAACATCGTGGAGGGTTAATTTGGTAGCCCTCACCCATTCTG
GTGTGGCTTCTTGAGAGGATTCCACCTCAAAATCATGAACCTGGCTGTTGATCAAAA
GAGAATTGGATTCTACTCTAAAGTCATAGGACTGGCAAAAGAAGCTAGCAGAAGAC
TCAACCTGGCCTCCCATAAACAGGACAGATTTCAGGTGATGGCAAAATGGATTCTACAT
CAACGGAGGCTATGAAAGCCATGAACAGATTCCAAAAAGAAAACCAAATTGGGAGGCCAAC
CCACAGAACAGCATTCTGGGCCAGGCTG**TAA**TCAGAATTGTCGTACATGCTAACAGC
ATTGCTTTTCCCCAAAATTAACACATTGTGGAGAAGTGATGATACTCTCCCCTACCTT
CCTCTCTCCATTCAAGCATTCAAAGTATATTCAATGAATTAAACCTTGCAGCAAGGGACC
TTAGATAGGCTTATTCTGACTGTATGCTTACCAATGAGAGAAAAAAATGCATTCCTGTAT
CATCCTTTCAATAAACTGTATTCAATTTGAAAAAAAAAAAAAAAAAAAAAA

FIGURE 155

MELIPTITSWRVLILVVALTQFWCGFLCRGFHLQNHELWLLIKREFGFYSKSQYRTWQKKLA
EDSTWPPINRTDYSGDGKNGFYINGGYESHEQIPKRKLKLGGQPTEQHFWARL

FIGURE 156

GTTCTCCTTCCGAGCAAATCCCAGGCATGGTGAATTATGAACGTGCCACACC**ATGAAG**
 CTCTTGCGAGGTAACTGTGCACCACACCTGGAATGCCATCCTGCTCCGTTCTGCTA
 CCTCACGGCGCAAGTGTGGATTCTGTGTCAGCCATCGCTGCTGCCGCCAGCCGGGGCCCC
 AGAACTGCCCTCCGTTGCTCGTAGTAACCAGTCAGCAAGGTGGTGTGCACGCCGG
 GCCCTCTCCGAGGTCCCAGGGTATTCCCTCGAACACCCGGTACCTAACCTCATGGAGAA
 CAACATCCAGATGATCCAGGCCACACCTCCGCCACCTCCACACCTGGAGGTCTGCAGT
 TGGCAGGAACCTCCATCCGGCAGATTGAGGTGGGGCCTTCAACGGCCTGGCCAGCCTAAC
 ACCCTGGAGCTGTCGACAACGGCTGACAGTCATCCCTAGCGGGGCCTTGAATACTGTC
 CAAGCTGCGGGAGCTCTGGCTTCGCAACAACCCATCGAAAGCATCCCCTTACGCCTTCA
 ACCGGGTGCCCTCCCTCATGCGCTGGACTTGGGGAGCTCAAGAAGCTGGAGTATATCTCT
 GAGGGAGCTTTGAGGGCTGTTAACCTCAAGTATCTGAACCTGGCATGTGCAACATTAA
 AGACATGCCAATCTCACCCCCCTGGTGGGGCTGGAGGAGCTGGAGATGTCAGGGAAACACT
 TCCCTGAGATCAGGCCTGGCTCCATGGCTGAGCTCCCTCAAGAAGCTGGGTATG
 AACTCACAGGTAGCCTGATTGAGCGGAATGCTTGTACGGGCTGGCTCACTTGTGGAAC
 CAAACTGGCCCACAATAACCTCTTGTACGGGCTTACCCGCTGAGGTAC
 TGGTGGAGTTGCATCTACACCAACCCCTGGAACGGTGTGATTGTGACATTCTGTGGCTAGCC
 TGGTGGCTTCGAGAGTATATACCCACCAATTCCACCTGCTGTGGCGCTGTGATGCTCCCAT
 GCACATGCGAGGCCGCTACCTCGTGAGGTGGACCGAGGCCCTCCAGTGTCTGCC
 TCATCATGGACGCACCTCGAGACCTAACATTCTGAGGGTGGATGGCAGAACTTAAGTGT
 CGGACTCCCCATGTCCTCCGTGAAGTGGTTGCTGCCAATGGGACAGTGCTCAGCCACGC
 CTCCGCCACCAAGGATCTGTCTCAACGACGGCACCTGAACTTCCACGTGCTGC
 TTTCAGACACTGGGTGTACACATGCACTGGTACGGCAACTCCAACGCC
 GCCTACCTCAATGTGAGCACGGCTGAGCTAACACCTCAACTACAGCTTCTCACCACAGT
 AACAGTGGAGACCACGGAGATCTGCCCTGAGGACACAACGCGAAAGTACAAGCCTGTTCTA
 CCACGTCACGGTACCGCCGATATACCAACCTTACACGGTGCTCATTCA
 CGTGTGCCAACGAGTGGCAGTACCCGCGACAGACACCAACTGACAAGATGCA
 GGATGAAGTCATGAAGACCACCAAGATCATCATTGGCTGCTTGTGGCAGTGACTCTGCTAG
 CTGCCGCATGGTATTGCTTCTATAAACTCGTAAGCGGACCCAGCAGCGGAGTACAGTC
 ACAGCCGCCGGACTGTTGAGATAATCCAGGTGGACGAAGACATCCCAGCAGCAACATCCGC
 AGCAGCAACAGCAGCTCCGTCCGGTGTACAGGTGAGGGGGCAGTAGTGCTGCC
 ATGACCATATTAACACTACAAACACCTACAAACCCAGCACATGGGGCCACTGGACAGAAA
 CAGCCTGGGGAACTCTGCAACCCACAGTCACCAACTATCTGAACCTTATATAATT
 CAGACCAACGAGTACAGGAAACTCAAAT**TGA**CTCCCTCCCCAAAAAAACTTATAAA
 TACCAAGGACAAGGTACAGGAAACTCAAAT**TGA**CTCCCTCCCCAAAAAAACTTATAAA
 GCAATAGAATGCACACAAAGACAGCAACTTTGTACAGAGTGGGGAGAGACTTTCTGTA
 TATGCTTATATATTAAAGTCTATGGGCTGGTAAAAAAACAGATTATATTAAATTAAAGA
 CAAAAAGTCAAAACA

FIGURE 157

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAAAAGPQNCPSCSNSQFSKVVC
RRGLSEVPQGIPSNTRYLNLMENNIQMIQADTFRHLHHLEVQLGRNSIRQIEVGAFNGLAS
LNTLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEY
ISEGAFEGFLNLKYLNLCMCNIKDMPNLTPIVGLEELEMMSGNHFPEIRPGSFHGLSSLKKLW
VMNSQVSLIERNNAFDGLASLVELNLAHNNLSSLPHDIFTPLRYLVELHLHHNPWNCDCDILW
LAWWLREYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFQCSAPFIMDAPRDLNISEGRMAEL
KCRTPPMSSVKWLLPNGTVLSHASRHPRISVLNDGTLFNVLLSDTGVTMVTNVAGNSN
ASAYLNVSTAELNTSNYSFFTWTETEISPEDTRKYKPVPTTSTGYQPAYTTSTVLIQ
TTRVPKQVAVPATDTTDKMQTSLDEVMKTTKIIIGCFVAVTLLAAAMLIVFYKLRKRHQQRS
TVTAARTVEIIQVDEDIPAATSAAATAAPSGVSGEAVVLPTIHDIINYNTYKPAHGAHWTE
NSLGNSLHPTVTTISEPYIIQTHTKDKVQETQI

FIGURE 158

CGCTCGGCACCAGCGCGCAAGG**ATG**GAGCTGGTTGCTGGACGCAGTGGGCTCACTTTCTTCAGCTCC
 TTCTCATCTCGTCCTTGCCAAGAGAGTACACAGTCATTAATGAAGCCTGCCCTGGAGCAGAGTGAATATCATG
 TGTGGGAGTGTGAATATGATCAGATTGAGTGCCTGCCCCGGAAAGAGGGAAGTCGTGGTTATACCAT
 CCCTTGCTGCAGGAATGAGGAGAATGAGTGTGACTCCTGCCTGATCCACCCAGGTTGACCATCTTGAAA
 GCAAGAGCTGCCGAAATGGCTCATGGGGGGTACCTGGATGACTCTATGTGAAGGGGTTCTACTGTGCAGAG
 TGCCGAGCAGGCTGGTACGGAGGAGACTGCATGCATGTGGCCAGGTTCTGCAGGCCAAAGGGTCAGATTT
 GTTGGAAAGCTATCCCCTAAATGCTACTGTGAATGGACCATTCATGCTAAACCTGGGTTGTATCCAAC
 GATTTGTCTGTTGAGTGTGGAGTTGACTACATGTGCCAGTATGACTATGTTGAGGTTGATGGAGAAC
 CGCGATGCCAGATCATCAAGCGTCTGTGGCAACGAGCGCCAGCTCCATTCAGAGCATAGGATCCTCACT
 CCACGTCCCTTCCACTCCGATGGCTCAAAGAATTGACGGTTCCATGCCATTATGAGGAGATCACAGCAT
 GCTCCTCATCCCTTGTTCATGACGGCACGTGCGCTTGCACAGGCTGGATCTTACAAGTGTGCCTGCTG
 GCAGGCTATACTGGCAGCGTGTGAAAATCTCTTGAAGAAAGAAACTGCTCAGACCTGGGGCCAGTC
 TGGGTACAGAAAATAACAGGGGCCCTGGGCTTATCAACGGACGCCATGCTAAAATTGGCACCGTGGTGT
 TCTTTGTAAACAACCTCTATGTTCTAGTGGCAATGAGAAAAGAACTTGCAGCAGAATGGAGAGTGGTCAGGG
 AAACAGCCCACATCTGCATAAAAGCCTGCCAGAACCAAGATTCAGACCTGGTGAAGAGGAGTTCTCCGAT
 GCAGGTTCAAGGGAGACACCATTACACCAGCTATACTCAGCGGCCCTCAGCAAGCAGAAACTGCAGAGTG
 CCCCTACCAAGAACGCCAGCCCTCCCTTGGAGATCTGCCATGGGATACCAACATCTGCATACCCAGCTCCAG
 TATGAGTGCATCTCACCCCTTACCGCCCTGGCAGCAGCAGGAGGACATGTCTGAGGACTGGAACTGGAG
 TGGGCGGCACCATCCTGCATCCCTATCTGCCGAAAATTGAGAACATCAGTCTCAAAGACCAAGGGTTGC
 GCTGCCGTGGCAGGCAGCCATCTACAGGAGGACCAGCAGGGTGCATGACGGCAGCCTACACAAGGGAGCGTGG
 TTCCTAGTCTGCAGCGGTGCCCTGGTGAATGAGCGACTGTGGTGGCTGCCACTGTGTTACTGACCTGG
 GAAGGTACCATGATCAAGACAGCAGACCTGAAAATCTACCGGGATGATGACCGGGATG
 AGAAGACCATCCAGAGCCTACAGATTCTGCTATCATTCTGCATCCAACTATGACCCCATCCTGCTGATGCT
 GACATGCCATCCTGAAGCTCTAGACAAGGCCGTATCAGCACCCGAGTCCAGCCCATCTGCCTGCTGCCAG
 TCGGGATCTCAGCACTCCCTCCAGGAGTCCCACATCACTGTGGCTGGATGCTCTGGCAGACGTGAGGA
 GCCCTGGCTCAAGAACACACTGCGCTCTGGGTGGTCACTGTGGTGAACCTGCTGCTGTGAGGAGCAG
 CATGAGGACCATGGCATTCCAGTGAAGCTGACTGAGACAGGAGGATCGCGGTGTGGCTGGAGCAG
 TGATATCTGCACTGCAGAGACAGGAGGATCGCGGTGTGGCTGGAGCAGACATCTCCTGAGCCACGCT
 GGCATCTGATGGGACTGGTCAAGCTGGAGCTATGATAAAACATGCAGCCACAGGCTCTTCACTGCCTT
 CACCAAGGTGCTGCCCTTAAAGACTGGATTGAAAGAAATATGAAA**TGA**ACCATGCTCATGCACCT
 CTGTTGAGAAGTGTTC
 TGATATCCGTCTGTACGTGTCAATTGCGTGAAGCAGTGTGGCCTGAAGTGTGATTGGCTGTGAACCTGG
 CTGTGCCAGGGCTCTGACTTCAGGGACAAAACCTCAGTGAAGGGTGAAGTAGACCTCATTGCTGGTAGGCTGAT
 GCCCGTCCACTACTAGGACAGCCAATTGGAAGATGCCAGGGCTTGCAAGAAGTAAGTTCTCAAAGAAC
 ATATACAAAACCTCCACTCCACTGACCTGGTGGCTTCCCCACTTCACTTACGATGCATCAGCTT
 ACCAGGGAAAGATCTGGGCTTCATGAGGCCCTTTGAGGCTCTCAAGTTCTAGAGAGCTGCCCTGGGACAGCC
 CAGGGCAGCAGAGCTGGGATGTGGTGCATGCCCTTGTGTACATGCCACAGTACAGTCTGGCCTTTCTCC
 CCATCTCTGTACACATTAAATAAGGGTGGCTCTGAACATACAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAA

FIGURE 159

MELGCWTQLGLTFQQLLISSLPREYTVINEACPGAEWNIMCRECCYEVDQIECVCPGKREVV
GYTIPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGTLDDFYVKGFYCAECRAGWYGGD
CMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRD
GDNRDGQIIKRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDG
TCVLDKAGSYKCACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTV
VSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKİSDLVRRRVLPMQVQSRETPLH
QLYSAAFSKQKLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRTCLRTGK
WSGRAPSCIPICGKIENTAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNE
RTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYRDDRDEKTIQSLQISATIILHPNYDPILLD
ADIAILKLLDKARISTRVQPICLAASRDLSTSFOESHITVAGWNVLADVRSPGFKNDSLRSG
VVSVVDSLLCEEQHEDHGIPVSVDNMFCASWEPTAPS DICTAETGGIAAVSFPGGRASPEPR
WHLMGLVWSWSYDKTCSHRLSTAFTKVLPFKDWIERNMK

FIGURE 160

ACCAGGCATTGTATCTCAGTTGTCATCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGA
 AGCTTTCTTGCCTGCAGTGAAGCAGAGAGATAGATATTATTACGTAATAAAAAAC**ATGGC**
 TTCAACCTGACTTCCACCTTCCTACAAATTCCGATTACTGTTGCTGTTGACTTTGTGCCT
 GACAGTGGTTGGGTGGGCCACCAGTAACACTTCGTGGTGCCATTCAAGAGAGTCCTAAAG
 CAAAGGAGTTCATGGCTAATTCCATAAGACCCCTCATTTGGGAAGGGAAAAACTCTGACT
 AATGAAGCATCCACGAAGAAGGTAGAACATTGACAACACTGTCCTCTGTCTCCTTACCTCAG
 AGGCCAGAGCAAGCTCATTCAAACCAGATCTCACTTGGAAAGAGGTACAGGCAGAAAATC
 CCAAAGTGTCCAGAGGCCGTATGCCCTCAGGAATGTAAGCTTACAGAGGGTCGCCATC
 CTCGTTCCCCACCGGAACAGAGAGAAACACCTGATGTACCTGCTGGAACATCTGCATCCCTT
 CCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTATCCACCCAGGCTGAAGGTAAAAAGT
 TTAATCGAGCCAAACTCTGAATGTGGGCTATCTAGAACGCCCTCAAGGAAGAAAATTGGGAC
 TGCTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTACAAGTGTGA
 GGAGCATCCCAAGCATCTGGTGGTGGCAGGAACAGCACTGGGTACAGGTTACAGTGCAGTG
 GATATTTGGGGTGTACTGCCCTAAGCAGAGAGCAGTTCAAGGTGAATGGATTCTCT
 AACAACTACTGGGGATGGGGAGGCCAAGACGGATGACCTCAGACTCAGGGTTGAGCTCCAAAG
 AATGAAAATTCCCGCCCTGCCTGAAGTGGTAAATATACAATGGCTTCCACACTAGAG
 ACAAAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTTACACCAAGTGTACGGAGTCTGG
 AGAACAGATGGGTGAGTAGTTGTTCTTATAAAATTAGTATCTGTGGAACACAATCCTTATA
 TATCAACATCACAGTGGATTCTGGTTGGC**TGA**CCCTGGATCTTGGTATGTTGG
 AAGAACTGATTCTTGTGCAATAATTGGCCTAGAGACTCAAATAGTAGCACACACATTA
 AGAACCTGTTACAGCTATTGTTGAGCTGAATTTCCTTTGTATTTCTTAGCAGAGCT
 CCTGGTGTAGAGTATAAACAGTTGTAACAAGACAGCTTCTTAGTCATTTGATCATG
 AGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGAT
 AAAATGAACGCTATTGAGGACTCTGGTTGAAGGGAGATTATTAAATTGAAGTAATATAT
 TATGGGATAAAAGGCCACAGGAATAAGACTGCTGAATGTCTGAGAGAACAGAGTTCT
 CGTCCAAGGTAGAAAGGTACGAAGATAACAATACTGTTATTCTGTACAATCATCT
 GTGAAGTGGTGGTGTCAAGGTGAGAAGGCCTCACAAAGAGGGAGAAAAGGCACGAATCA
 GGACACAGTGAACTTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTGGCTGCAAAGGCAG
 CAGTAGCTGAGCTGGTGCAGGTGCTGATGCCTCAGGGAGGACCTGCCAGGTATGCCT
 TCCAGTGATGCCACCAGAGAATACATTCTATTAGTTAAAGAGTTGTAAAATGA
 TTTGTACAAGTAGGATATGAATTAGCAGTTACAAGTTACATATTAACATAATAAAATA
 TGTCTATCAAATACCTCTGTAGAAAATGTAAAAAGCAAA

FIGURE 161

MGFNLTFHLSYKFRLLLTLCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLLGKGKT
LTNEASTKKVELNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRV
AILVPHRNREKHLMYLLEHLHPFLQRQLDYGIYVIHQAEGKKFNRAKLLNVGYLEALKEEN
WDCFIFHDVDLVPENDFNLYKCEEHPKHLVVGRNSTGYRLRYSGYFGGTALSREQFFKVNG
FSNNYWGWGGE-DDDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSR
VWR TDGLSSCSYKLVSVEHNPLYINITVDFWFGA

Important features:

Signal peptide:

amino acids 1-27

N-glycosylation sites:

amino acids 4-7, 220-223 and 335-338

Xylose isomerase proteins:

amino acids 191-201

FIGURE 162

CGTGGGCCGGGGTCGCGCAGCGGGCTGTGGCGCGCCCGAGGCACCGCCAGCTTCAGCTGCTGCCCTGGCC
GAGCTCCAGCTGCATTCCCTCCCGTCCGCCACGCTTCTCCGCTCCGGCCCCGCAATG
GCCCAGGCAGTGTGGTCGCGCTCGGCCATCCTCTGGCTGCCTGCCCTGGGC
CCCGCAGGGTGGCCGAGGCCTGTATGAACATCAATCTACCACCGATAGCCTGCCACCA
CGGGAGCGGTGGTGACCATCTCGCCAGCCTGGTGGCAAGGACAACGGCAGCCTGGCCCTG
CCCGCTGACGCCACCTTACCGCTTCACTGGATCCACACCCGCTGGTGTACTGGAA
GATGGAGAAGGGTCTCAGCTCACCATCCGTGTGGTCGGCACGTGCCCAGGGAAATTCCCGG
TCTCTGTCTGGGTCACTGCCGCTGACTGCTGGATGTGCCAGCCTGTGCCAGGGCTTGTG
GTCCTCCCCATCACAGAGTTCTCGTGGGGACCTGTTGTACCCAGAACACTCCCTACC
CTGGCCCAGCTCCTATCTCACTAACAGACCGCTTGAAAGTCTCCTCCACGACCGA
GCAACTCCTCAAGACGCCCTGTTCTACAGCTGGACCTCGGGACGGACCCAGATG
GTGACTGAAGACTCCGTGGTCTATTATAACTATTCCATCATCGGGACCTTCACCGTGAAGCT
CAAAGTGGTGGCGGAGTGGGAAGAGGTGGAGGCCAGGAGGGCTGTGAAGCAGAAGA
CCGGGACTTCTCCGCCCTCGCTGAAGCTGCAGGAAACCTTCGAGGCATCCAAGTGTGGGG
CCCACCTAATTCAAGACCTCCAAAAGATGACCGTGACCTGAACCTCTGGGGAGCCCTCC
TCTGACTGTGTGCTGGCGTCTAACGCTGAGTGCCTCCGCTGGAGGAAGGGAGTGCCACC
CTGTGTCCGTGCCAGCACAGCTAACCTGACCCACACCTCAGGGACCTGGGACTAC
TGCTTCAGCATCCGGGCCAGAATATCATCAGCAAGACACATCAGTACCAAGATCCAGGT
GTGGCCCTCCAGAATCCAGCCGGTGTCTTGCTTCCATGTGCTACACTTATCACTGTGA
TGTGCGCTTCATCATGTACATGACCTGCCAGGAAATGCCACTCAGCAAAAGGACATGGTGGAG
AACCCGGAGCCACCCCTCGGGGTAGGTGCTGCCAGATGTGCTGGGCCTTCTTGCT
GGAGACTCCATCTGAGTACCTGGAAATTGTTGCTGAGAACACAGGGCTGCTCCGCCCTCT
ATAAGTCTGTCAAAACTACACCGTG**TGAG**CACTCCCCCTCCCCACCCATCTCAGTGTAA
CTGACTGCTGACTTGGAGTTCCAGCAGGGTGGTGTGACCAACTGACCAAGGAGGGTTCAATT
TGCCTGGGCTGTTGGCTGGATCATCCATCTGTACAGTTCAGCCACTGCCACAAGCC
CCTCCCTCTGTGACCCCTGACCCAGCATTCAACCTCTGTACAGTCCAGCCACTGACA
TAAGCCCCACTCGGTACCAACCCCTGACCCCTACCTTGAAGAGGCTCGCAGGACT
TTGATGCTTGGGTGTTCCGTGTTGACTCTAGGTGGCCTGGCTGCCACTGCCATTCT
CTCATATTGGCACATCTGCTGCCATTGGGGTTCTCAGTTCTCCCCAGACAGCCCTAC
CTGTGCCAGAGAGCTAGAAAGAGTCATAAAAGGGTAAAAATCCATAACTAAAGGTTGTA
ACATAGATGGGCACACTCACAGAGAGAAGTGTGATGTACACACACACACACACA
CACACACACAGAAATATAAACACATGCGTCACATGGCATTTCAGATGATCAGCTCTGTA
TCTGGTTAAGTCGGTGTGGATGCACCCCTGCACTAGAGCTGAAAGGAATTGACCTCCA
AGCAGCCCTGACAGGTTCTGGGCCGGCCCTCCCTTGTGCTTGTCTGCAGTTCTGC
GCCCTTATAAGGCCATCTAGTCCCTGCTGGCTGGCAGGGCCTGGATGGGGGAGGACT
AATACTGAGTGAATGCAGAGTGCTTATAAAATACACCTTATTTATCGAAACCCATCTGTG
AAACTTCACTGAGGAAAAGGCCTTGCAGCGGTAGAAGAGGTTGAGTCAGGCGGGCGCGG
TGGCTACGCCGTGAACTCCAGCACTTGGGAGGCCAGGGGGTGGATCACGAGATCAGGA
GATCGAGACCAACCCCTGGTAACACGGTGAACACCCGCTCTACTAAAAAAATACAAAAAGTT
AGCCGGCGTGGTGGTGGTGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATG
GTGCGAACCCGGGAGGCCAGCTGCAGTGAGGCCAGATGGCGCCACTGCACTCCAGCCTGA
GTGACAGAGCGAGACTCTGTCTCCA

FIGURE 163

MAQAVWSRLGRILWLACLLPWAPAGVAAGLYEELNLTTDSPATTGAVVTISASLVAKDNGSLA
LPADAHLYRFHWIHTPLVLTGKMEGLSSTIRVVGHVPGEFPVSVWVTAADCWMQPVARGF
VVLPITEFLVGDLVVTQNTSLPWPSYLTKTVLKVSFLLHDPSNFLKTALFLYSWDFGDGTQ
MVTEDSVVYYNYSIIGTFTVKLKVVAEWEVEPDATRAVKQKTGDFSASLKLQETLRGIQVL
GPTLIQTFQKMTVTLNFLGSPPLETVCWRLKPECLPLEECEHPVSVASTAYNLHTFRDPGD
YCFSIRAENIISKTHQYHKIQVWPSRIQPAPVFAFPICALITVMLAFIMYMTLRNATQQKDMV
ENPEPPSGVRCCQMCCGPFLLETPSEYLEIVRENHGLLPPLYKSVKYTV

Important features of the protein:

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 339-362

N-glycosylation sites.

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

FIGURE 164

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACAGGGCACG**ATG**GCAC TGAGCTCCCAGATCT
GGGCCGCTTGCCTCCTGCTCCTCCTCGCCAGCCTGACCAGTGGCTCTGTTTCCA
CAACAGACGGGACAAC TTGCAGAGCTGCAACCCCCAGGACAGAGCTGGAGCCAGGCCAGCTG
GATGCCCATGTTCCAGAGGCAGAGGAGGCAGACACCCACTTCCCCATCTGCATTTCTGCT
GC GGCTGCTGT CATCGATCAAAGTGTGGGATGTGCTGCAAGACG**TAG**AACCTACCTGCCCTG
CCCCCGTCCCCTCCCTCCTTATT TATT CCTGCTGCCAGAACATAGGTCTT GGAATAAAA
TGGCTGGTTCTTTGTTCCA AAAAAAAAAAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA
AAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA

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FIGURE 165

MALSSQIWAACLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMMPMFQRRRRDTH
FPICIFCCGCCHRSKCGMCKT

FIGURE 166

CTGTCAGGAAGGACATCTGAAGGCTGCAATTGTTCTAGGGAGGCAGGTGCTGGCCTGGC
 CTGGATCTTCCACC**ATG**TTCCTGTTGCTGCCCTTTGATAGCCTGATTGTCAACCTTCTGGC
 ATCTCCCTGACTGTCCTCTCACCCCTCCTCGTTCATCATAGTGCCAGCCATTGG
 AGTCTCCCTTGATCCGAAACTCTACATGAAAAGTCTGTTAAAATCTTGCGTGGGCTA
 CCTTGAGAATGGAGCGAGGAGCCAAGGAGAAGAACCCAGCTTACAAGCCCTACACCAAC
 GGAATCATTGCAAAGGATCCCACCTCACTAGAAGAAGAGATCAAAGAGATTGTCGAAGTGG
 TAGTAGTAAGGCTCTGGACAACACTCCAGAGTTGAGCTCTGACATTCTACTTTGCC
 GGAAAGGAATGGAGACCATTATGGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAACTG
 GAGTCCTGGAACCTGCTGAGCAGAACCAATTATAACTCCAGTACATCAGCCTCGGCTCAC
 GGTCTGTGGGGTTAGGAGTGCTGATTGGTACTGCTTCTGCTGCCGCTCAGGATAGCAC
 TGGCTTCACAGGGATTAGCCTCTGGTGGGCCACAACGTGGTGGGATACTGCCAAAT
 GGGAGGTTAACGAAATTGAGTAAACATGTTACTTAATGTGTTACCGGATTCGCTGCG
 AGCGCTGACAGCCATCATCACCTACCATGACAGGGAAAACAGACCAAGAAATGGTGGCATCT
 GTGTGGCCAATCATACCTACCGATGATGTGATCATCTTGGCCAGCGATGGCTATTATGCC
 ATGGTGGGTCAAGTGCACGGGGACTCATGGGTGTGATTGAGAGGCCATGGTGAAGGCC
 CCCACACGTCTGGTTGAGCGCTCGGAAGTGAAGGATGCCACCTGGTGGCTAACAGACTGA
 CTGAACATGTGCAAGATAAAAGCAAGCTGCCATCCTCATCTTCCCAGAACGGAACTGCATC
 AATAATACATCGGTGATGATGTTCAAAAGGGAAAGTGGAAATTGGAGCCACAGTTACCC
 TGTTGCTATCAAGTATGACCCCTCAATTGGCGATGCCCTCTGGAACAGCAGCAAATACGGGA
 TGGTGACGTACCTGCTGCAATGATGACCAGCTGGGCATTGCTGCAAGCGTGTGGTACCTG
 CCTCCCATGACTAGAGAGGCAGATGAAGATGCTGTCCAGTTGCGAATAGGGTGAATCTGC
 CATTGCCAGGCAGGGAGGACTTGTGGACCTGCTGTGGATGGGGCTGAAGAGGGAGAAGG
 TGAAGGACACGTTCAAGGAGGAGCAGCAGAACAGCTGTACAGCAAGATGATCGTGGGAACCAC
 AAGGACAGGAGCCGCTCC**TGA**GCCTGCCCTCAGCTGGCTGGGCCACCGTGCAGGGTGC
 CGGGCTCAGAGCTGGAGTTGCCGCCGCCACTGCTGTGCTTCCAGACTCCAGGG
 CTCCCCGGGCTGCTCTGGATCCCAGGACTCCGGCTTCGCCAGGCCAGCGGGATCCCTGT
 GCACCCGGCGCAGCCTACCCCTGGTGGCTAAACGGATGCTGCTGGTGTGCAACCCAGGA
 CGAGATGCCTGTTCTTACAATAAGTCGTTGGAGGAATGCCATTAAAGTGAACCTCC
 CCTTGACGCTGTGCGGGCTGAGTGGTGGGAGATGTGGCATGGTCTTGTGCTAGAGAT
 GGCAGGCTACAAGAGTCTGTTATGCAAGCCGTGTGCCAGGGATGTGCTGGGGCGGCC
 CTCTCCAGGAAGGCACAGCTGAGGCAGCTGGCTGGCTGCCCTCAACATGCC
 CTTGGAGCTCTGCAGACATGATAGGAAGGAAACTGTCATCTGCAGGGCTTCAGCAAATG
 AAGGGTTAGATTTATGCTGCTGATGGGTTACTAAAGGGAGGGAGAGGCCAGGTG
 GGCGCTGACTGGGCATGGGAGAACGTGTGTTCGTACTCCAGGCTAACCTGAACCTCC
 ATGTGATGCGCGCTTGTGAATGTGTCGTTCCCATCTGTAATATGAGTCGGGG
 GAATGGTGGTGAACCTCACAGGGCTGTTGGGATTAAAGTGTGCGGGGTGAGTGA
 AGGACACATCACGTTCAAGTACAGGCCACAAAACGGGGCACGGCAGGC
 CTCAGAGCTGCACTGGCTTGGATTGTTCTGAGTAAATAACTGGCTGGTGA
 TGA

FIGURE 167

MFLLLPDFSLIVNLLGISLTVLFULLVFIIVPAIFGVSGIRKLYMKSLLKIFAWATLRME
RGAKEKNHQLYKPYTNGIIAKDPTSLEEEIKEIIRRSGSSKALDNTPEFELSDIFYFCRKGMETIMDDEVTKRFSAAELESWNLLSRTNMFQYISLRLTVLGVLIRYCFLPLRIALAFTG
ISLLVVGTTVVGYLPGFRKEFMSKHVHLMCYRICVRALTAITYHDRENPRNGGICVANHTSPIDVILASDGYYAMVGQVHGGLMGVIQRAMVKACPHVWFERSEVKDRHLVAKRLTEHVQDKSKLPILIFPEGTCINNTSVMMFKGSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMVTYLLRMMTSWAIVCSVWYLPPMTREADEDAVQFANRVKSAIARQGLVDLLWDGGLKREKVKDTEKEQQKLYSKMIVGNHKDRSRS

FIGURE 168

GCCCCCTCGAAACCAGGACTCCAGCACCTCTGGTCCC GCCCTCACCCGGACCCCTGGCCCTCA
CGTCTCCTCCAGGG**ATG** GCGCTGGCGGCTTGATGATGCCCTCGGCAGCCTCGGCCTCCAC
ACCTGGCAGGCCAGGCTGTTCCCACCATCCTGCCCTGGGCCTGGCTCCAGACACCTTGA
CGATACTATGTGGGTTGTGCAGAGGAGATGGAGGAGAAGGCAGCCCCCTGCTAAAGGAGG
AAATGGCCCACCATGCCCTGCTGCGGAATCCTGGGAGGCAGCCCAGGAGACCTGGGAGGAC
AAGCGTCGAGGGCTTACCTGCCCTGGCTCAAAGCCCAGAATGGAATAGCCATTATGGT
CTACACCAACTCATCGAACACCTGTACTGGGAGTTGAATCAGGCCGTGCGGACGGCGGAG
GCTCCCAGGAGCTCTACATGAGGCACTTCCCTCAAGGCCCTGCATTCTACCTGATCCGG
GCCCTGCAGCTGCTGCGAGGCAGTGGGGCTGCAGCAGGGACCTGGGAGGTGGTGTCCG
AGGTGTGGCAGCCTCGCTTGAAACCAAGAGGCTGGGGACTCTGTCGCTTGGCCAGT
TTGCCTCCAGCTCCCTGGATAAGGCAGTGGCCACAGATTGGGAGAAAGAGGCGGGCTGT
GTGTCTGCGCCAGGGTGCAGCTAGGGTCACAATCTGAGGGGCCTCCTCTGCCCTTG
GAAGACTCTGCTCTGGCCCTGGAGAGTTCCAGCTCTCAGGGTTGGCCC**TGA**AAGTCCA
ACATCTGCCACTTAGGAGCCCTGGAACGGTGACCTCATATGACGAAGAGGCACCTCCAG
CAGCCTTGAGAACAGAACATGGTCCGGACCCAGCCCTAGCAGCCTCTCCCCAACCAGG
ATGTTGGCCTGGGGAGGCCACAGCAGGGCTGAGGGAACTCTGCTATGTGATGGGACTTCCT
GGGACAAGCAAGGAAAGTACTGAGGCAGCCACTTGATTGAACGGTGTGCAATGTGGAGACA
TGGAGTTTATTGAGGTAGCTACGTGATTAAATGGTATTGCAGTGTGGA

FIGURE 169

MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGCAEEMEEKAAPLLKEEMAH
ALLRESWEAAQETWEDKRRGLTLPPGFKAQNGIAIMVYTNSSNTLYWELNQAVRTGGGSREL
YMRHFPEKALHFYLIRALQLLRGSGGCSRGPGEVVFRGVGSLRFEPKRLGDSVRLGQFASSS
LDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPPWKTLLLAPGEFQLSGVGP

FIGURE 170

GTGGCTTCATTCAGTGGCTGACTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCA
CCCTCATCTATATCCTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTG
GTCGGTTCCCGTTGGTGGGCCGTGACTTTCCCCCTGAAGTCAAAGTAAAGCAAGTTGACTC
TATTGTCTGGACCTTCAACACAAACCCCTTGTCAACCATAACAGCCAGAAGGGGGCACTATCA
TAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAG
CTCAGCAAACGTGAAGAAGAATGACTCAGGGATCTACTATGTGGGATATACAGCTCATCACT
CCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAG
TCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATG
GAACATGGGAAGAGGATGTGATTATACCTGGAAGGCCCTGGGCAAGCAGCCAATGAGTC
CCATAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGAGAAAGTGTATGACCTTCATCT
GCGTTGCCAGGAACCTGTCAGCAGAAACTCTCAAGCCCCATCCTGCCAGGAAGCTCTGT
GAAGGTGCTGCTGATGACCCAGATTCCCTCATGGTCCCTGTGTCTCCTGTTGGTGCCCT
CCTGCTCAGTCTTTGTACTGGGCTATTCTTGGTTCTGAAGAGAGAGAGACAAGAAG
AGTACATTGAAGAGAAGAAGAGAGTAGGGACATTGTCGGAAACTCCTAACATATGCCCAT
TCTGGAGAGAACACAGAGTACGACACAAATCCCTCACACTAATAGAACAAATCCTAAAGGAAGA
TCCAGCAAATACGGTTACTCCACTGTGGAAATACCGAAAAAGATGGAAAATCCCCACTCAC
TGCTCACGATGCCAGACACACCAAGGCTATTGCCTATGAGAATGTTATCTAGACAGCAGTG
CACTCCCTAACGTCTGCTCA

FIGURE 171

MAGSPTCLTLIYILWQLTGSAAAGPVKELVGSVGGAVTFPLSKVKQVDSIVWTFNTTPLVT
IQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHV
YEHLSKPVMTMGLQSNKNGTCVTNLTCMEHGEEDVIYTWKALGQAANESHNGSILPISWRW
GESDMTFICVARNPVSRNFSPIALKLCEGAADDPDSSMVLLCLLVPLLSSLFVLGLFLW
FLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPANTVYSTVEIP
KKMENPHSLLTMPDTPRLFAYENVI

FIGURE 172

CTGGTTCCCCAACATGCCTCACCCCATCTATATCCTTGGCAGCTCACAGGGTCAGCAGCC
TCTGGACCGTGAAAGAGCTGGTCGGTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTC
CAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTCAACACAACCCCTTGTCAACCATAAC
AGCCAGAAGGGGCACTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCA
GATGGAGGCTACTCCCTGAAGCTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGT
GGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACG
AGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTG
ACCAATCTGACATGCTGCATGGAACATGGGAAGAGGGATGTGATTTACCTGGAAGGCCCT
GGGGCAAGCAGCCAATGAGTCCCATAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGAG
AAAGTGATATGACCTTCATCTGCCTGCCAGGAACCCCTGTCAAGCAGAAACTTCTCAAGCCCC
ATCCTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCCCTCATGGTCCTCCT
GTGTCTCCTGTTGGTGCCTCCTGCTCAGTCTTTGTACTGGGCTATTCTTGGTTTC
TGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTGTCGGAA
ACTCCTAACATATGCCCTCATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAA
TAGAACAAATCCTAAAGGAAGATCCAGCAAATACGGTTACTCCACTGTGGAAATACGAAAAA
AGATGGAAAATCCCCACTCACTGCTCACGATGCCAGACACACCAAGGCTATTGCCTATGAG
AATGTTATCTAGACAGCAGTGCACTCCCCTAAGTCTGTCTCAAAAAAAAAAAAAAA

FIGURE 173

GAAAGACGTGGTCTGACAGACAGACAATCCTATTCCCTACCAAAATGAAGATGCTGCTGCT
GCTGTGTTGGGACTGACCCTAGTCTGTGTCATGCAGAAGAAGCTAGTTCTACGGGAAGGA
ACTTTAATGTAGAAAAGATTAATGGGAATGGCATACTATTATCCTGGCCTCTGACAAAAGA
GAAAAGATAGAAGAACATGGCAACTTAGACTTTCTGGAGCAAATCCATGTCTGGAGAA
TTCCTTAGTTCTAAAGTCCATACTGTAAGAGATGAAGAGTGCCTCGAATTATCTATGGTG
CTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGGATTCAATACATTACT
ATACCTAAGACAGACTATGATAACTTCTTATGGCTCACCTCATTAACGAAAAGGATGGGA
AACCTTCCAGCTGATGGGGCTCTATGCCGAGAACAGATTGAGTCAGACATCAAGGAAA
GGTTTGCACAACATATGTGAGGAGCATGGAATCCTAGAGAAAATATCATTGACCTATCCAAT
GCCAATCGCTGCCTCCAGGCCGAGAATGAAGAACATGCCCTGAGCCTCCAGTGTGAGTGGAC
ACTTCTCACCAGGACTCCACCATCATCCCTCCTATCCATACAGCATCCCCAGTATAAATT
TGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCAATTCCAGTCTATCAACATGTTACC
TAGGATACCTCATCAAGAACAAAGACTTCTTAAATTCTCTTGATAACACCCTGACAAT
TTTCATGAAATTATTCCCTTCCTGTTCAATAATGATTACCCTGCACTTAA

FIGURE 174

MKMLLLCLGLTLVCVHAEVASSTGRNFNVEKINGEWHTIILASDKREKIEEHGNFRLFLEQ
IHVLENSLVLKVHTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLI
NEKDGETFQLMGLYGREPDLSSDIKERFAQLCEEHGILRENIIDLMSNANRCLQARE

FIGURE 175

GGCTCGAGCGTTCTGAGCCAGGGGTGACC**ATG**ACCTGCTGCGAAGGATGGACATCCTGCAA
TGGATTCA~~G~~CCTGCTGGTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATA~~C~~CTCTAATTG
TCAGCTTAGTTGAGGAAGACCAATTTCCTAAAACCCATCTTGCTTGAGTGGTGGTTC
CCAGGAATTATAGGAGCAGGTCTGATGCCATTCCAGCAACAACAATGTCCTTGACAGCAAG
AAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTCTTCATCATTTCAGTGTGATCA
CAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTAAAAGGT CCTCTC
ATGTGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTCATTGAAAAACATCAGTGA
CATTCA~~T~~CCAGAAC~~T~~CCACTGCAGTGGTTTCAATGACTCTTGCGACCTCCTACTG
GTTTCAATAAACCCACCAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTCCAC
TTCGATTCTGAAGAAAACAAACATAGGCTTATCCACTTCTCAGTATTAGGTCTATTGCT
TGTTGGAATTCTGGAGGTCTGTTGGGCTCAGTCAGATA~~G~~T~~C~~ATCGGTTCC~~T~~GGCTGTC
TGTGTGGAGTCTAAGCGAAGAAGTCAAATTGTG**TAG**TTAATGGGAATAAAATGTAAGTA
TCAGTAGTTGAAAAAAAAAAA

FIGURE 176

MTCCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWFPGIIGAGLMA
IPATTMSLTARKRACCNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPLMCNSPSNSNA
NCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSEENKHRL
IHFSVFLGLLLGVILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

FIGURE 177

GTCGAATCCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACC**ATG**AGGCT
GTCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTGCTGCTACCAAGGCCCATGCTCTTGTCT
GCCCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGC GGTAACCTC
CAAGTTGCCAAACTTAATCCACCTCCAGAAGCTCTGCAGCCAAGTTGGAAGTGAAGCACTG
CACCGATCAGATATCTTTAAGAAACGACTCTCATTGAAAAAGTCCTGGTGGAA**TAG**TGAA
AAAATGTGGTGTGACATGTAAAAATGCTAACCTGGTTCAAAGTCTTCAACGACACC
CTGATCTCACTAAAAATTGTAAAGGTTAACACGTTGCTTAATAAATCACTGCCCTGC

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FIGURE 178

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNLOVAKLNPPPEALAAKLEV
KHCTDQISFKKRLSLKKSWWK

FIGURE 179

ATCCGTTCTCTGCCTGCCAGCTCAGGTGAGCCCTGCCAAGGTGACCTCGCAGGACACTGG
TGAAGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTG
GAGCAGATCCGTGGGCTGCAGACCCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCTC
GAACTGTGAC**ATG**GAGAGAGTGACCCCTGGCCCTCTCCTACTGGCAGGCCTGACTGCCTTGG
AAGCCAATGACCCATTGCCAATAAAGACGATCCCTCTACTATGACTGGAAAAACCTGCAG
CTGAGCGGACTGATCTGCGGAGGGCTCCTGCCATTGCTGGATCGCGCAGTTCTGAGTGG
CAAATGCAAATACAAGAGCAGCCAGAACGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCAC
TCATCACTCCAGGCTCTGCCACTACTTGC**TGA**GCACAGGACTGGCCTCCAGGGATGGCCTGA
AGCCTAACACTGGCCCCCAGCACCTCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTC
TCTCCAAGGGCAGGCTGTTAGGCCCTTCTGATCAGGAGGCTTCTTATGAATTAAACTCG
CCCCACCACCCCTCA

FIGURE 180

MERVTLALLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCK
YKSSQKQHSPVPEKAIPPLITPGSATTC

FIGURE 181

GGAGAAGAGGTTGTGGACAAGCTGCTCCGACAGAAGGATGTCGCTGCTGAGCCTGCC
 TGGCTGGGCCTCAGACCGGTGGCAATGTCCCCATGGCTACTCCTGCTGCTGGTTGTGGCCTC
 CTGGCTACTCGCCCGCATCCTGGCTTGGACCTATGCCCTATAACAACTGCCGCCGGCTCC
 AGTGTTCACAGCCCCAAAACGGAACCTGGTTGGGTACCTGGCCTGATCACTCCT
 ACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTCGCCACCTATTCCCAGGGCTTACGGT
 ATGGCTGGGTCCCATCATCCCCTCATCGTTATGCCACCCGTACACCATCCGGTCTATCA
 CCAATGCCTCAGCTGCCATTGCACCCAAGGATAATCTTCATCAGGTTCTGAAGCCCTGG
 CTGGGAGAAGGGATACTGCTGAGTGGCGGTGACAAGTGGAGGCCACCGTCGGATGCTGAC
 GCCCGCCTTCCATTCAACATCCTGAAGTCCTATATAACGATCTCAACAAGAGTGCAAACA
 TCATGCTTGACAAGTGGCACCTGGCCTCAGAGGGCAGCAGTCGTCTGGACATGTTGAG
 CACATCAGCCTCATGACCTTGGACAGTCTACAGAAATGCATCTCAGCTTGACAGCCATTG
 TCAGGAGAGGCCAGTGAATATATTGCCACCATCTGGAGCTCAGTGCCTTGTAGAGAAAA
 GAAGCCAGCATATCCTCCAGCACATGGACTTCTGTATTACCTCTCCATGACGGCGGC
 TTCCACAGGGCTGCCGCTGGTCATGACTCACAGACGCTGTACCGGGAGCGCGTCG
 CACCCCTCCCCACTCAGGGTATTGATGATTTTCAAAGACAAAGCCAAGTCCAAGACTTGG
 ATTTCATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTCAGATGAGGAT
 ATAAGAGCAGAGGCTGACACCTCATGTTGGAGGCCATGACACCACGCCAGTGGCTCTC
 CTGGGTCTGTACAACCTTGCAGGGCACCCAGAATACCAGGAGCGCTGCCACAGGAGGTGC
 AAGAGCTCTGAAGGACCGCGATCTAAAGAGATTGAATGGGACGACCTGGCCAGCTGCC
 TTCCTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTCATCTCCG
 ATGCTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTGCC
 TCATCGATATTATAGGGTCCATCACAACCAACTGTGTGGCCGGATCCTGAGGTCTACGAC
 CCCTTCCGCTTGACCCAGAGAACAGCAAGGGAGGTACCTCTGGCTTTATTCTTCTC
 CGCAGGGCCCAGGAACCTGCATCGGGCAGGCAGTCGCATGGGGAGATGAAAGTGGCTGG
 CGTTGATGCTGCTGCACCTCCGGTCTGCCAGACCAACTGAGCCCCCAGGAAGCTGGAA
 TTGATCATGCGGCCGAGGGCGGGCTTGGCTGCGGGTGGAGCCCCTGAATGTAGGCTTGCA
 GTGACTTCTGACCCATCCACCTGTTTGCAGATTGTCATGAATAAACGGTGCTGTCAA

FIGURE 182

MSLLSLPWLGRLPVAMSPWLLLLLVGSWLLARILAWTYAFYNNCRRQLQCFQPQPKRNWFWG
HLGLITPTEEGLKDSLQMSATYSQGFTVWLGPPIIPFIVLCHPDTIRSITNASAAIAPKDNLF
IRFLKPWLGEGLLSGGDKWSRHRRLTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGS
SRLDLMFEHISLMTLDSLQKCIFSFDHCQERPSEYIATILELSALVEKRSQHILQHMDFLYY
LSHDGRRFHRCRLVHDFTDAVIREERRTLPTQGIDDFFKDKAKSKTLDFIDVLLLSKDEDG
KALSDEDIRAEADTFMFGGHDTTASGLSWVLVNLARHPEYQERCRQEVQELLKDRDPKEIEW
DDLAQLPFLTMCVKESLRILHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVW
PDPEVYDPFRDPENSKGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLHFRFLPDHT
EPRRKLELIMRAEGGLWLVEPLNVGLQ

FIGURE 183

CAACAGAAGCCAAGAAAGGAAGCCGTCTATCTTGTGGCGATC**ATG**TATAAGCTGGCCTCCTGC
TGTTTGCTTTCACAGGATTCTTAAATCCTCTTATCTCTTCCTCTCCTGACTCCAGGGA
AATATCCTTCAACTCTCACGACCTCATGAAGACGCCGCTTAACCTCCGGAGGAGCTAGAAA
GAGCTTCCCTCTACAGATATTGCCAGAGATGCTGGGTGCAGAAAGAGGGGATATTCTCAGG
AAAGCAGACTCAAGTACCAACATTTAACCCAAGAGGAAATTGAGAAAGTTTCAGGATT
CTCTGGACAAGATCCTAACATTACTGAGTCATCTTGGCCAGAATCTGAAACCATA
AGAACACGTGAGACTCCTGATTGCTCTGAAATACTGTGTC**TGA**AGTGAATAAGCATCTGT
TAGTCAGCTCAGAAACACCCATCTTAGAATATGAAAAATAACACAATGCTGATTGAAAAC
AGTGTGGAGAAAAACTAGGCAAACACACCCCTGTTATTGTTACCTGGAAAATAATCCTCT
ATGTTTGCACAAAAAAAAAAAAAA

FIGURE 184

MYKLASCCLLFTGFLNPLLSLPLLDREISFQLSAPHEDARLTPEELERASLLQILPEMLGA
ERGDILRKADSSTNIFNPRGNLRKFQDFSGQDPNILLSHLLARIWKPYKKRETPDCFWKYCV

FIGURE 185

GAACATTTAGTCCAAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGAT
GGGGTTGCTGGTTAAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCA
CCACCTCCGCCAGGAACTGCAGGCCACCTGTCTGCAACCCAGCTGAGGCC**ATG**CCCTCCCC
AGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCT
CCAGCTTCCCTGAGCCCTGAAACACCAAGAGACTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCA
GCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCGGAAAGATGGAGGTCAAGCAGA
AGGGGCAGAGGATGAACTGGAAGTCCGGTTAACGCCCTTGATGTTGGAATCAAGCTGT
CAGGGGTTCACTTACAGCACAGCCAGGCCCTGGGGAAAGTTCTTCAGGACATCCTCTGG
GAAGAGGCCAAAGAGGCCAGCCGACAAG**TGA**TCGCCACAAGCCTTACTCACCTCTCT
AAGTTAGAAGCGCTCATCTGGCTTTCGCTTGCTGCAGCAACTCCCACGACTGTTGTA
CAAGCTCAGGAGGCATAAAATGTTCAAAGTGA

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FIGURE 186

MPSPGTVCSLLLGMWLDDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPEDG
GQAEGAEDLEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADKO

FIGURE 187

CGGCCACAGCTGGCATGCTCTGCCTGATGCCATCCTGCTGTATGTCCTCGTCCAGTACCTC
GTGAACCCCAGGGTGCTCCGCACGGACCCAGATGTCAAGAATATGAACACGTGGCTGCTGT
TCCTCCCCCTGTTCCCGGTGCAGGTGCAGACCCCTGATACTCGTGCATCGGGATGCTCGTG
CTCCTGCTGGACTTCTTGGCTGGTCACCTGGCCAGCTGCTCATCTTCCACATCTACCT
GAGTATGTCCCCCACCTAACGCCCCGATCCCCCAAGGCTGGTGGTCAGAGCTGCTCATC
TTACACCTCTACTTGAGTATGTCCTAACCTGAGCCCCCACGCCCTGGGCCAGAGTCTT
GTCCCCCGTGTGCGATGTGTTCAAGGTCAGCCTCTCCCAGAAAGTGAGATCATGGACAAAAA
GGCAAATCACAGGAAGAAATTAAATCCATGAGGACCCAGCAGGCCAGCAAGAAGCTGAAC
TCACGCCGAGACCTGCAGGAGTGGTGCAGGTGCTTGAAGTAACAAGTTAAAATGTTAGA
GACAATGGAATGGAATCTATTAGGAAGAACAGGACATTATGAAATAAGGACAGGTGGACTT
CCAAAAACACAAGTAGAAATTCTAACATGAAATATATTACAGGCAGGTACCCACTAACCA
AACAACTGAAGCGAGAGCTGTGGTCTTGCTTCAGGTGGCACAGCGGTAGGCGGTC
AGTCATGTTGCTGAACGACGGAGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGT
AACAAACAACCTCCCTGCTCCTGGCACCCAGCCGTTGGTCATGGTGGGCCAGCTGCAAAGCG
TCTTCCATTCTCTGGCAGTGGTGGCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTGGCCA
ACGGGCAGCAGAGTGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTGGCCA
ACCCCTGGTCAGGGCAGAGGGAGTTGGGTGGTCAGGCTCTGGCTCACCTCCATCTCCAGA
GCATCCCCCTGCCTGCAGTTGGCAAGAACGCCAGCTCAGAATGAACACACCCCCACCAAGA
GCCTCCTGTTCATAACACAGGTTACCCCTACAAACCACAGCTGCCCCACACAACCTGGGAT
GTTTTAAAACACACACACCTCTAACGCATATCTTACAGTCAGTCACTGTTGTCCTGCCTGAGGGTTGA
ATTTTTTTAATGAAAGTGAATGAAATCACTGGATTAAATCCTACGGACACAGAGCTGAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 188

MNTWLLFLPLFPVQVQTLIVVIIGMLVLLDFLGLVHLGQLLIFHIYLSMSPTLSRSPQGW
VVRAAHLTPLLEYVPNPEPPTPGARVFVPRVRMCSGSASPRSEIMDKGKSQEEIKSMRTQQ
AQQEAEELTPRPAGVVPGA

FIGURE 189

GGAGTGCAGATGGCATCCTCGTTCTCCAGACAAGCTGCAAGACGCTGACC**ATG**GCCAAG
 ATGGAGCTCTCGAAGGCCTCTCTGGCAGCGGACACTCCTATCTGCCATCCTCAGCATGCT
 ATCACTCAGCTCTCCACAACATCCCTGCTCAGCAACTACTGGTTGTGGCACACAGAAGG
 TGCCCAAGCCCCTGTGCGAGAAAGGTCTGGCAGCCAAGTGCTTGACATGCCAGTGTCCCTG
 GATGGAGATAACCAACACATCCACCCAGGAGGTGGTACAATACAACACTGGGAGACTGGGGATGA
 CCGGTTCTCCTCCGGAGCTTCCGGAGTGGCATGTGGCTATCCTGTGAGGAAACTGTGGAAG
 AACCAGGGAGAGGTGCCAGTTTCAATTGAACCTACACCACAGCCAAGAGAGGGTGGAAAG
 GGACTACTGGAATTGCCACGTTGCAAGGCCATGTCACCCCCACTCTCCGATTGGAGGGAA
 CGCGTTGATGGAGAAGGCTCCCTCCCTCCCTCCCTGGGCTTGTGGCAAAAATCCTA
 TGGTTATCCCTGGAACGCAGATCACCTACATCGGACTTCAATTCATCAGCTCCTCCTGCT
 ACTAACAGACTTGCTACTCACTGGAACCCCTGCCTGTGGCTCAAACGTAGCGCCTTGCTG
 CTGTTCTCTGTCAGGTCTCCTGGGATGGTGGCCACATGATGTATTACAAGTC
 TTCCAAGCGACTGTCAACTGGGTCCAGAAGACTGGAGACCACATGTTGGAATTATGGCTG
 GGCCTCTACATGGCCTGGCTCCTCACCTGCTGCATGGCGTGGCTGTCACCACCTCA
 ACACGTACACCAGGATGGTGGCTGGAGTTCAAGTGCAG**TAG**TAAGAGCTCAAGGAAAC
 CCGAACTGCCTACCACATCACCACATCAGTGGTCCCTCGCGGCTGTCAAGTGCAGCCCCAC
 CGTGGGTCTTGACCAGCTACCACCAAGTATCATAATCAGCCATCCACTCTGTCTTGAGG
 GAGTCGACTTCTACTCCGAGCTGCGGAACAAGGGATTCAAAGAGGGCCAGCCAGGAGCTG
 AAAGAACGAGTTAGGTCACTGTAGAGGAAGAGCAGTGTAGGAGTTAAGCGGGTTGGGA
 GTAGGCTTGAGCCCTACCTACACGTCTGCTGATTATCAACATGTGCTTAAGCCAACATCCG
 TCTCTTGAGCATGGTTTAGAGGCTACGAATAAGGCTATGAATAAGGTTATCTTAAGTC
 CTAAGGGATTCCCTGGGTGCCACTGCTCTTTCTACAGCTCCATCTGTTACCCAC
 CCCACATCTCACACATCCAGAATTCCCTTACTGATAGTTCTGTGCCAGGTTCTGGGC
 TAAACCATGGAGATAAAAGAAGAGTAAACACTTCCCGACCTTAAGGATCTGAAA

FIGURE 190

MAKMELSKAFSGQRTLLSAILSMLSLSFSTTSLLSNYWFGTQKVPKPLCEKGLAAKCFDMP
VSLDGDTNTSTQEVVQYNWETGDDRFSFRSGMWLSCEETVEEPGERCRSFIELTPPAKR
GEKGLLEFATLQGPCHPTLRFGGKRLMEKASLPSPPLGLCGKNPMVIPGNADHLHRTSIHQL
PPATNRLATHWEPCWLWAQTERLCCCFLCPVRSPGDGGPHDVFTSLPSDCQLGSRRLETTCLE
LWLGLLHGLALLHLLHGVGCHHLQHVHQDGAGVQVQA

FIGURE 191

AACTGGAAGGAAAGAAAGAAAGGTCA GCTTGGCCCAGATGTGGTTACCCCTGGTCTCCTG
TCTTTATGTCTTCTCCTCTTCCTATTCTGTCA TCTCCCTCACTTAAGTCTCAGGCCTGTCA
GCAGCTCCTGTGGACATTGCCATCCCCTCTGGTAGCCTTCAGAGCAAACAGGACAACCTATG
TTATGGATGTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACC ATCTGTGCTTCTGT
GATCTCTATGACAGAGGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAAATCTGGCATG
AGATGGCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCCTGCCCTATTCCCTCCCAA
GTCTGTTCTCTTATTGTCAACCTCAGCACAA CAGGCTGGCGCAATGGCATTACAGAGAAAG
CAATCTGTGTGGCTAGTGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTGT
AGCCACCTCCCTGTCAGCCAGTATTAACATGTCCTCCCTGCCCTGCCGTAGATTCA
GACATTGCCCTGTGTGCCACCAACCAGGACTTCCCTGGCTTGGCATCCCTGGCT
CTCCTGGTACCCAGCAAGACGTCTGTTCCAGGGCAGTGTAGCATCTTCAAGCTCCGTTACT
ATGGCGATGCCATGATGTTACAATCCCAC TTGCCTGAATAATCAAGTGGAAAGGGAAAGCA
GAGGGAAATGGGCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCC TGAGGAAAAACCAA
GGGAAGCAACAGGAAC TTCTGCAACTGGTTTATCGGAAAGATCATCCTGCCTGCAGATGC
TGTTGAAGGGCACAAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTGAAGGAA
ATAGAACAGTCTGCTGGAGTCAGACCTGGAATTCTGATTCCA AACTCTTATTACTTGGG
AAGTCACTCAGCCTCCCCTAGCCATCTCCAGGGTGACGGAAACCCAGTGTATTACCTGCTGG
AACCAAGGAAACTAACAAATGTAGGTTACTAGTGAATACCCAAATGGTTCTCCAATTATGCC
CATGCCACCAAAACAATAAAACAAAATTCTCTAACACTGAAA

FIGURE 192

MWLPLGLLSLCLSPLPILSSPSLKSQACQQLWTLPSPLVAFRANRTTYVMDVSTNQGSGME
HRNHLCFCFDLYDRATSPPLKCSLL

FIGURE 193

GTAGCGCGCTTGGGTCTCCCGCTGCCGCTGCCGCCCGCTGGGTCTGGAGGCCAGGAGCAGTCACGCC
 CGGCC **ATG** GCAGGCATCAAAGCTTGATTAGTTGCTCTTGGAGGAGCAATCGGACTGATGTTTGATGCTT
 GGATGTGCCCTTCCAATATAACAACAAATACTGGCCCTCTTGTCTATTGCTATTTTACATCCTTCACCTATTCC
 ATACTGCATAGCAAGAAGATTAGTGGATGATAAGATGCTATGAGTAACGCTTGTAAAGAACCTGCCATCTTC
 TTACAACGGGCATTGCGTGTAGCTTGGACTCCCTATTGTATTGCCAGAGCACATCTGATTGAGTGGGA
 GCTTGTGCACTTGTCTCACAGGAAACACAGTCATCTGCAACTATACTAGGCTTTCTGGTCTTGGAA
 CAATGACGACTTCAGCTGGCAGCAGTGG**TGA**AAAGAAATTACTGAACATATTGTCAAATGGACTTCCGTCA
 GTTGGCCATTACGCACACAGGAGATGGGCAGTTAATGCTGAATGGTATAGCAAGCCTTGGGGTATT
 GGTGCTCCCTCTACTTTTATTGTAAGCATACTATTTCACAGAGACTTGCTGAAGGATTAAAAGGATTTCT
 CTTTGGAAAAGCTTGAUTGATTCACACTTATCTATAGTATGCTTTTGTGGTGTCCCTGCTGAATTAAAT
 TTATGTGTTTCTGTAGGTGATTTTTTGGAATCAATATGCAATGTTAACACATTAAATGTAATCA
 TTTGCATTGGTAGGAATTCAAATCCGGCGCTCTTACTGGTCAAGTACATCTTCTCTTAAATT
 TAGGCTCATTATTACAAAAAATTAAAAAATAGTTTCACTGAGCATGTCAGTCAGGATGACATCACTCCAAATGTTAG
 CAGACATACAGACGGTGGCATACGTTAGACTGTACTGCAAAATATAGCTGCATTACCTCAGAG
 GGGCCAAGTGTAAATGCCATGCCCTCGGTAAAGGGTTGTTACTGGTAGACAGATGTTGTGGATTG
 AAAATTATTGAAATTGCTACAGAGGAGTGCTTCTCTCAATTGTTAGAAGAATTATGTTAAACCTTA
 AGGTAAGGGTGTAAAACATTGAGATAAGGTTTATTGTTAGTGTAGAGTGAGTTGAATGT
 GGGAAAGAAATGACATTGAAATTCCAGTTTGAATCCTGTTCTATTATACTGAAATTGTTGATCTCCTATC
 AACCTTCATGTTTACCTGTAAAATGGACATACATGGAAACCACACTGATGAGGGACAGTTGATGTTGC
 ATCATATATGCCAGAAAACCTCCTCTGCTCCTCCTTGAATTGTTGATGTTGATATATACATAAA
 TAACCTTCAAATATACTGTTAACACTAGTAGAAGTGTACTTACCTGGAAAATAATTGCTATGCCGTACATT
 CAGAGTCCCCCTCCCTGCAAGGCCTGCCATGATTAACAAGTAATTGTTAGTCTTACAGATAATTGCA
 TTAACAGTTAAGATTAGACCATGGTAATAGTAGTTCTTATTCTCAAGGTTATATGCAATTAAAG
 TATTGTTAAGACAAGTTCCGTATACCTCTGAACGTGTTGATTGAGTCATCATGATAGATCTGCTGTT
 CCTTATAAAAGGCATTGTTGAGTTAATGCAAAGTAGCCAAGTCCAGTATATGCAAGCTCAGAAACAT
 ACCTGACCAAAAAATCCCAGTAACCAGGCATGATCAATTATAGTGGCTTACATCTAATAATTACAGGA
 CTTTTTCAGGAGTGGTTATAAAACATCAAGTGGTCTGACAGTTGTTAGGATATTGTTGATG
 TTATTGAGTACTACATAAAATTATTGCCCACAGGAAACTCAGTAATCATGACAGCTGCTGTTG
 TTATGAAAGTTATTCTCAAGAAAATGGAATAATTGGGATTGTTAGCTTACTAAAGATGCCTAA
 AGCCACAGGTTTATTGCTTAAGCCATGACTTTAGATGAGATGACGGGAAGCAGGAGCAAATATCG
 GCGTGTGGCTGGAGCCCTCCACTGGAGGCTGAAAGTGGCTTGTGGTATTATAATGTCAGATTCAAGAGGAA
 GGTGCAGGTACACATGAGTTAGAGAGCTGGTGGAGACAGTTGGAACTCTTGTGCTTGTGATCTACTGGACTT
 TTTTTGCAAGGAAAGTGCATTCTGCTGCCCTTCTGTTCTGGATGTCAGTGCAGTGCACGTGCTACTG
 TTTTATCCACTGGCACAGACTTTCTAACAGCTCGTATTATTTCTATATACTAATTGCAATTGGCAGCATT
 GTGTCTTGACCTTGTATACTAGCTTGACATAGTGTCTCTGATTCTAGGCTAGTTACTGAGGATATGAAT
 TTTCCATAGAATATGCACTGATAACACATTACATTCTATGAAAGAAAATTGATGATGAAACAATAA
 AGATTAAATATCTATTAAAAAA

FIGURE 194

MAGIKALISLSFGGAIGLMFLMLGCALPIYNKYWPLFVLFFYIILSPIPYCIARRLVDDTDAM
SNACKELAIFLTTGIVVSAFGLPIVFARAHLIEWGACALVLTGNTVIFATILGFFLVFGSND
DESWQQW

FIGURE 195

FIGURE 196

MDFLLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPH
NLSGLLGLSLRYNSLSELRAGQFTGLMQLTWLYLDHNHICSVQGDAFQKLRRVKELTLSSNQ
ITQLPNTTFRPMPNLRSDLSYNKLQALAPDLFHGLRKLTLLHMTRANAIQFPVRIIFQDCRS
LKFLDIGYNQLKSLARNSFAGLFKLTELHLEHNDLVKVNFAHFPRLISLHSLCLRRNKVAIV
VSSLWDWWNLEKMDLSGNEIEYMEPHVFETVPHLQSLQDSNRLTYIEPRILNSWKS LTSIT
LAGNLWDCGRNVCALASWLSNFQGRYDGNLQCASPEYAQGEDVLDavyAFHLCEDGAEPTSG
HLLSAVTNRSDLGPPASSATTIADGGEQHDGTFEPATVALPGGEHAENAVQIHKVVTGTMA
LIFSFLIVVLVLYVSWKCFPASLRQLRQCFVTQRRKQKQTMHQMAAMSAQEYYVDYKPNH
IEGALVIINEYGSCCTCHQQPARECEV

FIGURE 197

GTGCAAGGAGCCGAGGCAGA**ATG**GGCGTCCTGGCCGGTCTGCTGTGGCTGCAGCTCTGC
GCACTGACCCAGGCGGTCTCAAACACTGGTCCCCAACACGGACTTCGACGTGCAGCAA
CTGGAGCCAGAACCGGACCCGTGCCCGGGGCCGTTGAGTTCCC GGCGACAAGATGG
TGTCAGTCCTGGTGAAGAAGGTACGCCGTCTCAGACATGCTCCTGCCGCTGGATGGGAA
CTCGTCCTGGCTTCAGGAGCCGGATTCGGCCTCAGACGTGGGCTCGCACCTGGACTGTGG
CGCGGGCGAACCTGCCGTCTCCGCACTCTGACCGCTTCTCCTGGCATGACCCGCACCTGT
GGCGCTCTGGGGACGAGGCACCTGGCCTTTCTCGTGGACGCCGAGCGCGTGCCTGCCGC
CACGACGACGTCTTCTTCGCCTAGTGCCTCCTCCCGTGGGCTCGGCCCTGGCGCTAG
CCCCGTGCGTGTCCGCAGCATCTCGCCTCTGGCCGGACGTTACGCGCGACGAGGACCTGG
CTGTTTCTGGCGTCCC CGCGGGCCGCCTACGCTTCCACGGGCCGGCGC**TGA**CGGTG
GGCCCCGAGGACTGCGCGAACCGTCGGCTCGTCTGCGAACGCGGAGGCGCAGCCGTG
GATCTGCCGCGGCCCTGCTCCAGCCCC

FIGURE 198

MGVLGRVILLWLQLCALTQAVSKLWVPNTDFVAANWSQNRTPCAGGAVEFPADKMVSVLVQE
GHAVSDMILLPLDGEVLASGAGFGVSDVGSHLDGAGEPAVFRDSDRFSWHDPHLWRSGDEA
PGLFFVDAERVPCRHDDVFPPSASFRVGLGPASPVRVRSISALGRTFTRDEDLAVFLASR
AGRLRFHGPGALSVPEDCADPSGCVCGNAAQPWICAALLQP

FIGURE 199

ATCGCATCAATTGGGAGTACCATCTTCCTC**ATG**GGACCAGTGAAACAGCTGAAGCGAATGTT
TGAGCCTACTCGTTGATTGCAACTATCATGGTGCTGTTGTGTTGCACTTACCCGTGTT
CTGCCTTTGGTGGCATAACAAGGGACTTGCACTTATCTTCTGCATTTGCAGTCTTGGCA
TTGACGTGGTACAGCCTTCCTCATACCATTGCAAGGGATGCTGTGAAGAAGTGTGTTGC
CGTGTGTCTTGCAT**TAA**TTCATGCCAGTTATGAAGCTTGGAGGCACATGGACAGAAC
CTGGTGGACAGTTGTAACTATCTCGAAACCTCTGTCTACAGACATGTGCCTTTATCT
TGCAGCAATGTGTTGCTTGATTGAAACATTGAGGGTTACTTTGGAAGCAACAATACAT
TCTCGAACCTGAATGTCAGTAGCACAGGATGAGAAGTGGTTCTGTATCTTGTGGAGTGGAA
TCTTCCTCATGTACCTGTTCCCTCTGGATGTTGTCCCCTGAATTCCCATGAATACAAAC
CTATTCAACAGCAACAGCAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAA

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FIGURE 200

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCASFWWNKGLALIFCILQSLALTWYSLSFIP
FARDAVKKCFAVCLA

FIGURE 201

TTGAGCGCAGGTGAGCTCTGCGCGTCCGGGGCGTCCTCCAGTCACCCCTCCGCCGTTACCCGCCGCG
 CCGAGGGAGTCTCCTCCAGACCCCTCCCGTGCCTCAAACATAACGGACTGAACGGATCGCTGCAGGG
 GGGAGAGAAAATTAGGGGGAGAAAGGACAGAGAGAGCAACTACCATCCATAGCCAGATAGATTATCTTACACTG
 AACTGATCAAGTACTTGAAA**ATG**ACTTCGAAATTATCTTGGTGCCTTCATACTTGCTGCAGTGAGTCTTC
 AACCACTTCTCCAAGTACAGACAGCAAAGGTTCTACTAGTTCTTGATGGATTCCGTTGGGATTACT
 TATATAAAGTCCAAGCCCCATTTCATTATATTATGAAATATGGTGTACGTGAAGCAAGTTACTAATGTT
 TTTATTACAAAAACCTACCTAACCATTTACTTGTAACGGCTCTTGCAGAGAACATGGGATTGTTGC
 AAATGATATGTTGATCCTATTGGAACAAATCTTCTCTGGATCACATGAATATTATGATTCCAAGTTT
 GGGAAAGAAGCGACACCAATATGGATCACAAACAGAGGGCAGGACATACTAGTGGTGCAGCCATGGCCCCGA
 ACAGATGAAAAAATACATAAGCGCTTCTACTCATTACATGCCTTACAATGAGTCAGTTCAATTGAAGATAG
 AGTTGCCAAATTGTTGAATGGTTACGTCAAAGAGGCCATAATCTGGTCTCTATTGGGAAGACCC
 ATGACATGGGCCACCATTTGGGACCTGACAGTCCGCTCATGGGCCGTGTCATTCAAGATATTGACAAGAAGTAA
 GGATATCTCATACAAATGCTGAAAAAGGCAAGTTGGAACACTCTGAACACTAATCATCACAAGTGAATGG
 ATGACGCGAGTCTGAGGAAAGGTTAATAGAACTTGACAGTACCTGGATAAGACCACTAACCCGTGATTG
 ATCAATCTCCAGTAGCAGCCATCTGCCAAAGAAGGTAATTGATGAAGTCTATGAAGCCTAACGCT
 CATCCTAATCTTACTGTTACAAAAAGAACGTTCCAGAAAGGTGGCATTACAAATACAACAGTCGAAATTCA
 ACCAATCATAGCAGTGGCTGATGAAGGGTGGCACATTACAGAATAAGTCAGATGACTTCTGTTAGGCAACC
 ACGGTTACGATAATGCGTTAGCAGATATGCATCCAATATTTAGCCCAGGTCCTGCCTCAGAAAGAATT
 TCAAAAGAAGCCATGAACCTCACAGATTGACCCACTACTATGCCACCTCCTCAATATCACTGCCATGCCACA
 CAATGGATCATTCTGGAATGTCCAGGATCTGCTCAATTCAAGCAGGCCAAGGGTGGCCTTATACACAGAGTA
 CTATACTCCCTGGTAGTGTAAACCAGCAGAATATGACCAAGAGGGTCAACCCATTTCATAGGGTC
 TCTCTGGCAGCATTATAGTGAATTGATTTGTAATTTCATTAAGCATTAATTCAAGTCAAATACCTGC
 CTTACAAGATATGCATGCTGAAATAGCTCAACCATTATTACAAGCT**TAAT**GTTACTTGAAAGTGGATTG
 CATA TTGAAGTGGAGATTCCATAATTATGTCAGTGTAAAGGTTCAAATTCTGGAAACCAAGTTCCAAACATCTGC
 AGAAACCATTAAGCAGTTACATATTAGGTATACACACACACACACACACACACGGACCAAA
 ATACTTACACCTGCAAAGGAATAAGATGTGAGAGTATGTCCTATTGTTACTGTAGCATAGGGATAGATAAG
 ATCCCTGTTATTGACTTGGCGCAGATAATGTATAATTAGCAACTTGCACACTATGTAAGTACCTTATAAT
 ATTGCACTTTAAATTCTCTCTGATGGTACTTTAATTGAAATGCACTTATGGACAGTTATGCTTATAAC
 TTGATTGAAAATGACAACCTTTGCACCCATGTCACAGAAACTACTGTTACGATTGTCATAACTGAAGGAAATT
 TCTAATAATCCCGAATAATGAACATAGAAATCTATCTCCATAAAATTGAGAGAAGAAGGGTGAATAGTGTGA
 AAATTAAATGTGATAACCTTGAACCTTGAATTGGAGATGTATTCCCAACAGCAGAAATGCAACTGTGGGCAT
 TTCTGTCTATTCTTCCAGAGAACGTGGTTTCATTATTTCCCTCAAAGAGAGTCAAATACTGACAG
 ATTGTTCTAAATATATTGTTCTGTCATAAAATTATTGTGATTCTGTGATGAGTCATATTACTGTGATTTC
 TAATAATGAAGACACCATGAATAACTTTCTTCTATATAGTTCAAGCAATGGCCTGAATAGAAGCAACCAGGCA
 CCATCTCAGCAATGTTCTCTGTTGTAATTATTGCTCCTTGAAAATTAAATCACTATTACATTAA
 AAATCAAATTGGATAAAAAAAAAAAAAAA

FIGURE 202

MTSKFILVSFILAALSLSTTFSIQLDQQKVLLVSFDGFRWDYLYKVPTPHFHYIMKYGVHVK
QVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEETPIW
ITNQRAGHTSGAAMWPGBTDKIHKRFPTHMPYNESVSFEDRVAKIVEWFTSKEPINLGLLY
WEDPDDMGHHLGPDSPLMGPVISIDKKLGYLIQMLKAKLWNTLNLIITSDHGMTQCSEER
LIELDQYLDKDHYTLIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKEDVPERWHYKYN
SRIQPIIAVADEGWHLQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTD
LYPLLCHLLNITAMPNGSFVNQDLIINSAMPRVVPTQSTILLPGSVKPAAEYDQEGSYPYF
IGVSLGSIIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

Signal Peptide:

amino acids 1-22

Transmembrane Domain:

amino acids 429-452

N-glycosylation sites:

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-
372, 382-385, 389-392

Somatomedin B Domain:

amino acids 69-85

Sulfatase protein Region:

amino acids 212-241

FIGURE 203

GGATTTGTGATCCCGATTGCTCCCACGGCGGGACCTTGTAACTGCAGGGAGGCCAG
 GACAGGCCACCCTGCGGGCGGGAGGCAGCCGGGTGAGGGAGGTGAAGAAACCAAGACGC
 AGAGAGGCCAAGCCCCTGCCTGGTCACACAGCAAAGGAGGCAGAGCCAGAACTCACAA
 CCAGATCCAGAGGCAACAGGGAC**ATG**GCCACCTGGACGAAAAGGCAGTCACCGCAGGGCC
 AAGGTGGCTCCCGCTGAGAGGATGAGCAAGTCTTAAGGCACCTCACGGCGTGGGAGACGA
 CTACCATGCCTGGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGG
 AGCAGCCACCACCCACACCAGTCTCAGGCAGGAAGGCAGAGCTGCAGCCCTGACGTTGCC
 CCTGCCCTGGCCCCGCACCCAGGGCCCCCTGACTTCAGGGCATGTTGAGGAAACTGTT
 CAGCTCCACAGGTTTCAGGTATCATCATCTGCTTGGTGGTCTGGATGCCCTGGTGC
 TTGCTGAGCTCATCCTGGACCTGAAGATCATCCAGCCGACAAGAATAACTATGCTGCCATG
 GTATTCCACTACATGAGCATCACCATCTGGTCTTTTATGATGGAGATCATCTTAAATT
 ATTTGTCTCCGCTGAGTTCTTCACCACAAGTTGAGATCCTGGATGCCCGTGGTGG
 TGGTCTCATTCATCCTGGACATTGTCCTCCTGTTCCAGGAGCACCAGTTGAGGCTCTGGC
 CTGCTGATTCTGCTCCGGCTGTGGCGGGTGGCCCGGATCATCAATGGGATTATCATCTCAGT
 TAAGACACGTTAGAACCGCAACTCTTAAGGTTAAACAGATGAATGTACAATTGGCCGCCA
 AGATTCAACACCTTGAGTTAGCTGCTCTCCGGATGGCTATGGGAATGAAAGAATCCGACTTCTACTCT
 AACCTGTAAGGAGAAGCTCTCCGGATGGCTATGGGAATGAAAGAATCCGACTTCTACTCT
 CACACAGCCACCGTGAAAGCTCTGGAGTAAATGTGCTGTACAGAAGAGAGAGAAGGAAG
 CAGGCTGGCATGTCAGTGGCTGGTGTACAGAGAACCTGACAGTCAGTCACTGGCCAGTTA
 TCACTTCAGATTACAAATCACACAGAGCATCTGCCTGTTCAATCACAAGAGAACAAACC
 AAAATCTATAAGATATTCTGAAAATATGACAGAATTGACAAATAAAGCATAAACGTGTA
 AAAAAAAAAAAAAAAAAAAAAAA

FIGURE 204

MATWDEKAVTRRAKVAPAERMSKFLRHFTVVGDDYHAWNINYKKWENEEEEEEQPPPTPV
SGEEGRAAAPDVAPAPGPAPRAPLDFRGMLRKLFRSHRFQVIIICLVVLDAALLVIAELILDL
KIIQPDKNNYAAMVFHYMSITILVFFMMEIIFKLFVFRLLSSFTTSLRSWMPVVVVVSFILDI
VLLFQEHQFEALGLLILLRLWRVARIINGIIISVKTRSERQLLRLKQMNVQLAAKIQHLEFS
CSEKPLD

FIGURE 205

CGGCTCGAGCTCGAGCCGAATCGGCTCGAGGGGCAGTGGAGCACCCAGCAGGCCAAC**AT**
GCTCTGTCGTGCCGTACGTGCCGTATCGGGGAAGGCCAGACCGAGTTCCAGTACTTTG
 AGTCGAAGGGGCTCCCTGCCGAGCTGAAGTCATTTCAGTCAGTGTCTTCATCCCCTCC
 CAGGAATTCTCACCTACGCCAGTGGAAAGCAGAAAATTGTACAAGCTGGAGATAAGGACCT
 TGATGGCAGCTAGACTTTGAAGAATTGTCATTATCTCCAAGATCATGAGAAGAAGCTGA
 GGCTGGTGTAAAGATTTGGACAAAAAGAATGATGGACGCATTGACGCCAGGAGATCATG
 CAGTCCTGCCGGACTTGGAGTCAAGATATCTGAACAGCAGGCCAGAAAAATTCTCAAGAG
 CATGGATAAAAACGGCACGATGACCATCGACTGGAAAGGAGTGGAGAGACTACCACTCC
 ACCCGTGGAACATCCCCGAGATCATCCTCTACTGGAAGCATTCCACGATCTTGATGTG
 GGTGAGAATCTAACGGTCCCGATGAGTTCACAGTGGAGGAGAGGCAGACGGGATGTGGT
 GAGACACCTGGTGGCAGGAGTGGGGCAGGGCGTATCCAGAACCTGCACGCCCGCTGG
 ACAGGCTCAAGGTGCTCATGCAGGTCATGCCTCCCGCAGCAACACATGGCATCGTTGGT
 GGCTTCACTCAGATGATTGAGAAGGAGGGCCAGGTCACTCTGGCAGGAGGATCCTGGCAGAGAGGGGG
 CGTCCCTAAAATTGCCCGAATCAGCCATCAAATTATGCCATGAGCAGATCAAGCGCC
 TTGTTGGTAGTGACCAGGAGACTCTGAGGATTACGAGAGGCTGTGGCAGGGTCCTGGCA
 GGGGCCATCGCCAGAGCAGCATCTACCCAATGGAGGTCTGAAGACCCGGATGGCCTGCG
 GAAGACAGGCCAGTACTCAGGAATGCTGGACTGCGCAGGAGGATCCTGGCAGAGAGAGGGGG
 TGGCCGCTTCTACAAAGGCTATGCCCCAACATGCTGGCATCATCCCTATGCCGCATC
 GACCTTGCACTACGAGACGCTCAAGAATGCCCTGGCTGCAGCACTATGCACTGAACAGCGC
 GGACCCCGCGTGGTGTGCTCTGGCCTGTGGCACCATGTCCAGTACCTGTGGCAGCTGG
 CCAGCTACCCCTGGCCCTAGTCAGGACCCGGATGAGGCCAGGCTCATATTGAGGGCGCT
 CCGGAGGTGACCATGAGCAGCCTCTCAAACATATCCTGCCAGGAGGGGCTTCGGGCT
 GTACAGGGGCTGGCCCAAACCTCATGAAGGTACATCCCAGCTGTGAGCATCAGCTACGTGG
 TCTACGAGAACCTGAAGATCACCTGGCGTGCAGTCGG**TGA**CGGGGGAGGGCCCG
 GCAGTGGACTCGCTGATCCTGGGCCAGCCTGGGTGTGCAGCCATCTCATTCTGTGAATG
 TGCAACACTAAGCTGTCTCGAGCCAAGCTGTGAAAACCCTAGACGCACCCGCAGGGAGGGT
 GGGGAGAGCTGGCAGGCCAGGGCTGTGCTGACCCAGCAGACCCCTCTGTTGGTIC
 AGCGAAGACCACAGGCATTCTTAGGGTCAGGGTCAGCAGGCTCCGGGCTCACATGTGTA
 GGACAGGACATTTCTGCAGTCAGGCTGCAATAGTGAGGCTGGAGCCTGGAGGGCCGGCTTAGT
 TCTTCCATTTCACCTTGAGCCAGCTGTGTTGGCCACGGGCTCTGGCTCTGGTCTGCCGTGC
 ATCTCCCTGTGCCCTCTGCTGCTGCCCTGCTGAGGTAAAGTGGAGGAGGGCTACAG
 CCCACATCCCACCCCTCGTCCAATCCCATATCCATGATGAAAGGTGGAGGTACGTGCC
 CCCAGGCCCTGACTCCCAACCTACAGCATTGACGCCAACTTGGCTGTGAAGGAAGAGGAAG
 GATCTGGCTTGTTGACTGGCATCTGAGCCCTGCTGATGGCTGGGCTCTGGCATGCT
 TGGGAGTGCAGGGGCTGGGCTGCCCTGCTGAGGATGGGCCACCTCAGAACCAAACACT
 TCCCCACTGTGGCATGAGGGCAGTGGAGCACCAGTTGAGGGCGAAGGGCAGAGCGTTGT
 GTGTTCTGGGGAGGGAAAGGAAAAGGTGTTGGAGGCCTAATTATGGACTGTTGGAAAAGGG
 TTTTGTCCAGAAGGACAAGCCGGACAAATGAGCGACTCTGTGCTTCCAGAGGAAGACGAGG
 GAGCAGGAGCTGGCTGACTGCTCAGAGTCTGTTGACGCCCTGGGGTCTGCCAAC
 CCAGCAGGGCGCAGCGGGACCAGCCCCACATTCCACTTGTGTCAGTGCTTGGAAACCTATT
 ATTTGTATTATTGAAACAGAGTTATGCTCTAAACTATTTTATGTTGATGTACCTCCC
 GCTTGTCTTTCAAGTTCTTATTGATGGCTGCTTGTGAAAGGTGGAATCCAGTTATT
 AAGCCCCCAGTGGGATGGGAGGAGGAGGAGAAGGGGGCTGGGCCGCTGCAGTCACAT
 CTGTCCAGAGAAATTCTTTGGGACTGGAGGCAGAAAAGCGGCCAGAAGGCAGCAGCCCTG
 GCTCCTTCTTGGCAGGGTGGGAAGGGCTGCCCTGGGCTTAGGATTGAGGTGTTGA
 CTGGGGCGTGGAGAGAGAGGGAGGAACCTCAATAACCTGAAAGGTGGAATCCAGTTATT
 CTGCGCTGCAGGGTTCTTATTCACTCTTCTGAATGTCAAGGCAGTGAGGTGCCTCT
 CACTGTGAATTGTGGTGGCGGGGCTGGAGGAGAGGGTGGGGGCTGGCTCCGTCC
 CAGCCTCTGCTGCCCTGCTTAACAATGCCGCCAAGTGGCAGCCTCACGGTTGCACCTCC
 ATTCCACCAAGAATGACCTGATGAGGAAATCTCAATAGGATGAAAGATCAATGCAAAAATT
 GTTATATATGAACATATAACTGGAGTCGTAAAAAGCAAATTAAAGGAAAGAATTGGACGTTAG
 AAGTTGTCAATTAAAGCAGCCTCTAATAAAAGTTGTTCAAAGCTGAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 206

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSYRQWKQKIVQAGDKD
LDGQLDFEEFVHYLQDHEKKLRLVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEKILK
SMDKNGTMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMW
WRHLVAGGGAGAVSRTCTAPLDRLKVLMQVHASRSNNMGIVGGFTQMIREGGARSLWRGNGI
NVLKIAPESAIKFMAYEQIKRLVGSDQETLRIHERLVAGSLAGAIAQSSIYPMEVLKTRMAL
RKTGQYSGMLDCARRILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNAWLQHYAVNS
ADPGVFVLLACGTMSSTCGQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFG
LYRGLAPNFMKVIPAVSISYVVYENLKITLEGVQSR

Important features:

Signal peptide:

amino acids 1-16

Transmembrane domain:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation site.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

FIGURE 207

GGAAGGCAGCGGAGCTCCACTCAGCCAGTACCCAGATA CGCTGGAACCTTCCCCAGCC**AT**
GGCTTCCTGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAG
 CAATTGCACTCATCATTGGCTTGGTATTCAGGGAGACACTCCATCACAGTCACACTGTGTC
 GCCTCAGCTGGAACATTGGGAGGATGGAATCCTGAGCTGCACTTTGAACCTGACATCAA
 ACTTTCTGATATCGTGTACAATGGCTGAAGGAAGGTGTTTAGGCTTGGTCCATGAGTTCA
 AAGAAGGCAAAGATGAGCTGTCGGAGCAGGATGAAATGTTCAGAGGCCGGACAGCAGTGTGTT
 GCTGATCAAGTGATAGTGGCAATGCCTCTTGC GGCTGAAAAACGTGCAACTCACAGATGC
 TGGCACCTACAAATGTTATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATA
 AAAC TGGAGCCTCAGCATGCCGGAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTG
 CGGTGTGAGGCTCCCCGATGGTCCCCCAGCCCACAGTGGTCTGGCATCCCAAGTTGACCA
 GGGAGCCAAC TTCTCGGAAGTCTCCAATACCAGCTTGAGCTGAAC TCTGAGAATGTGACCA
 TGAAGGTTGTGCTGTGCTCTACAATGTTACGATCAACAAACACATACTCCTGTATGATTGAA
 AATGACATTGCCAAAGCAACAGGGATATCAAAGTGA CAGAATCGGAGATCAAAGGCGGAG
 TCACCTACAGCTGCTAAACTCAAAGGCTCTGTGTCTCTTCTTGC CATCAGCT
 GGGCACTTCTGCCCTCTCAGCCCTTACCTGATGCTAAA**TAA**TGTGCCTGGCCACAAAAAAG
 CATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTCACCACCAGATATGACCTAG
 TTTTATATTCGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAAACAAAGAGCA
 AGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAAGATAATCTATCTCAA
 GACATATTAGAAGTTGGAAAATAATTGTA CACTAGACAAGTGTGTTAAGAGTGATAAG
 TAAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTCACCT
 GGGGAGTGAGAGGACAGGATAGTGCATGTTCTTGTCTGAATT TAGTTATGTGCTG
 TAATGTTGCTCTGAGGAAGCCCCTGGAAAGTCTATCCAAACATATCCACATCTTATATTCCA
 CAAATTAAGCTGTAGTATGTACCTAAGACGCTGCTAATTGACTGCCACTCGCAACTCAGG
 GGC GGCTGCATTTAGTAATGGGTCAAATGATTCACTTTATGATGCTCCAAAGGTGCCT
 TGGCTTCTCTTCCAACTGACAAATGCCAAAGTTGAGAAAATGATCATAATTAGCATAA
 ACAGAGCAGTCGGGACACCGATTTATAAAACTGAGCACCTTCTTTAAACAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 208

MASLGQILFWSIISIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDI
KLSDIVIQWLKEGVGLVLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNVQLTD
AGTYKCYIITSKGKGNANLEYKTGAFSMPEVNVDYNASSETLRCEAPRWFPQOPTVWASQVD
QGANFSEVSNTSFELNSENVTMKVSVLYNVTINNTYSCMIENDIAKATGDIKVTESIJKRR
SHLQLLN SKASLCVSSFFAISWALLPLSPYLMK

FIGURE 209

GAATTGTAGAACAGCGGCGTTGCC **ATGGCGCGCTCTGGGCAGGTGTTGGCTCTGGT**
 GCTGGTGGCCGCTCTGTGGGCTGGCACGCAGCCGCTGCTGAAGCAGGCCTCCGCCGGCCTGC
 AGCGGGTTCATGAGCCGACCTGGGCCAGCAGTTGCTACAGGAGATGAAGACCCTTCTTG
 AATACTGAGTACCTGATGCCCTTCCTCAACCAGTGTGGATCCCTCTATTACCTCAC
 CTTGGCATCGACAGATCTGACCCCTGGCTGTGCCCATCTGTAACTCTGGCTATCATCTCA
 CACTGATTGTTGGAAGGCCCTGGAGAAGATATTGGTGGAAAACGTAAGTTAGACTACTGC
 GAGTGCAGGCAGCTGTGGATCTCGACATACCTGTGTTAGTCCTCCCAGAACCCAT
 CTCCCCAGAGTGGGTGAGGACACGCCCTTCCCCTGCCTTCCTGCAGCTGTT
 GCTTCCTGTGGCCATCAGAGTCCCTCCCTGGACAGTCTGGAGAAAGACAGAGGCTGG
 GTTGGGAT**TGA**AGACCAGACCCATCTGAGCCCTCCTCCAGCCCTGTGTTAGCTCCTACT
 GGCATGGCTGAGCTCAGACCCCTCGATTTCTGCCTATTATCCAGGAGCAGTTGCTGGCAT
 GGTGCTCACCGTGATAGGAATTCACTCTGCATCACAAGCTCAGTGAGTAAGACCCAGGGC
 AACAGTCTACCCCTTGAGTGGCGAACCCACTCCAGCTCTGCTGCCTCCAGGAAGCCCT
 GGGCCATGAAGTGTGGCAGTGAGCGGATGGACCTAGCACTCCCTCTGGCCTAGCTT
 CCTCCTCTTATGGGATAACAGCTACCTCATGGATCACAATAAGAGAACAGAGTGAAG
 AGTTTGTAACCTCAAGTGTGTTAGCTGCTGGGGATTAGCACAGGAGACTCTACGCTCA
 CCCTCAGCAACCTTCTGCCAGCAGCTCTCCCTGCTAACATCTCAGGCTCCAGCCCA
 GCCACCATTACTGTGGCTGATCTGGACTATCATGGTGGCAGGTTCCATGGACTGCAGAACT
 CCAGCTGCATGGAAAGGGCCAGCTGCAGACTTGAGGCCAGAAATGCAAACGGGAGGCCTCTG
 GGACTCAGTCAGAGCGCTTGGCTGAATGAGGGTGGAACCGAGGGAGAGGTGCGTCGGA
 GTGGCAGATGCAGGAAATGAGCTGTCTATTAGCCTGCCTGCCACCCATGAGGTAGGCAG
 AAATCCTCACTGCCAGCCCTTAAACAGGTAGAGAGCTGTGAGCCCCAGCCCCACCTGAC
 TCCAGCACACCTGGCGAGTAGTAGCTGTCAATAATCTATGTAACAGACAAAAAA
 AAA

210/330

FIGURE 210

MAASLGQVLALVLVAALWGGTQPLLKRASAGLQRVHEPTWAQQLQEMKTLFLNTEYLMF
LNQCGSLLYYLTIASTDLTAVPICNSLAIIFTLIVGKALGEDIGGKRKLDYCECGTQLCGS
RHTCVSSFPEPISPEWVRTRPFPILPFPLQLFCFLVAIRVPFPWTWRKTEAGVWD

FIGURE 211

CTTCTGTAGGACAGTCACCAGGCCAGATCCAGAAGCCTCTAGGCTCCAGCTTCTGTG
 GAAGATGACAGCAATTATAGCAGGACCCTGCCAGGCTGTCGAAAAGATTCCGCAATAAAACT
 TTGCCAGTGGAAAGTACCTAGTGAAACGGCTAACAGATGCCACTTCTTCATGTCCCAGGCT
 TGAGGCCCTGTGGTCCCCATCCTGGGAGAAGTCAGCTCCAGCACC**ATGA**AAGGGCATCCTCG
 TTGCTGGTATCACTGCAGTGTTGCAGCTGTAGAATCTCTGAGCTGCGTGCAGTGTAAAT
 TCATGGAAAAATCCTGTCAACAGCATTGCCTCTGAATGTCCCTCACATGCCAACACCAG
 CTGTATCAGCTCCTCAGCCAGCTCCTCTAGAGACACCAGTCAGATTATACCAGAATATGT
 TCTGCTCAGCGGAGAACTGCAGTGAGGAGACACACATTACAGCCTTCACTGTCCACGTGTCT
 GCTGAAGAACACTTCATTTGTAAGCCAGTGCTGCCAAGGAAAGGAATGCAGCAACACCAG
 CGATGCCCTGGACCCTCCCTGAAGAACGTGTCCAGCAACGCAGAGTGCCCTGCTTGTATG
 AATCTAATGGAACTCCTGTCGTGGAGCCCTGGAAATGCTATGAAGAAGAACAGTGTGTC
 TTTCTAGTTGCAGAACCTAACAGATTGAGTCTAACAGTCTCGTGTGAAAGGCTGTTC
 CAACGTCAGTAACGCCACCTGTCAGTCCCTGTCTGGTAAAACAAGACTCTGGAGGAGTCA
 TCTTCGAAAGTTGAGTGTGCAAATGTAAACAGCTAACCCCCACGTCTGCACCAACCACT
 TCCCACAACGTGGCTCCAAAGCTTCCCTTACCTCTTGGCCCTGCCAGCCTCCTCTCG
 GGGACTGCTGCCCT**TGA**GGTCTGGGCTGCACTTGCCAGCACCCATTCTGCTTCTG
 AGGTCCAGAGCACCCCTGCGGTGCTGACACCCCTTTCCCTGCTCTGCCCCGTTAACTGC
 CCAGTAAGTGGAGTCACAGGTCTCAGGCAATGCCGACAGCTGCCCTGTTCTCATTATTA
 AAGCACTGGTTATTCACTGCCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 212

MKGILVAGITAVLVAAVESLSCVQ CNSWEKSCVNSIASECPSHANTSCISSASSSLETPVR
LYQNMFCSAENCSEETHITAFTVHVS AEEHFHFV SQCCQGKECSNTSDALDPPLKNVSSNAE
CPACYESNGTSCRGKPWKC YEEE QCVFLVAELKNDIESKSLVLKGCSNVSNATCQFLSGENK
TLGGVIFRKFECANVNSLTPTSAPTTSHNVGSKASLYLLALASLLL RGLLP

FIGURE 213

GGCCTCGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGGAGCGAAGGTAGGAGGCA
GGGCTTGCCTCACTGCCACCCCTCCAACCCCAAGAGCCCAGCCCC**ATG**GTCCCCGCCGCC
GCGCGCTGCTGTGGTCCTGCTGAATCTGGTCCCCGGCGGGGGCCAAAGGCCTG
ACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTACGCTTGCCCCATGACCCGCAG
CTACCGGAGCACCGCCCGGACTGGTCTCCCCGAAGACAAGGATAATCCTAGAGGACGAGA
ATGATGCCATGGCCGACGCCGACCGCCTGGCTGGACCAGCGGCTGCCGAGCTTGGCGCC
ACGGTGTCCACCGGCTTAGCCGGTGTCCGCCATTAACGAGGAGGATGGGTCTTCAGAAGA
GGGGTTGTGATTAATGCCGGAAAGGATAGCACCAGCAGAGAGCTTCCCAGTGCAGCTCCCA
ATACAGCGGGGAGTTCCAGCACGAGGTTATAGCCAATAGTCAGGAGCCTGAAATCAGGCTG
ACTTCAAGCCTGCCCGCTCCCCGGAGGTCTACTGAGGACCTGCCAGGCTCGCAGGCCAC
CCTGAGCCAGTGGTCCACACCTGGTCTACCCGAGCCGGTGGCGTCACCCCTACCCACAG
CCATGCCATCTCCTGAGGATCTGCCGGTGGTGTGATGCCCTGGGCCGTGGCACTGCCAC
TGCAAGTCGGCACCATGAGCCGGAGCCGGTGGGAAGCTGCACGCCCTTCCGGCGCCT
TCGAGTTGGCGCTGAGCCAGCTCCGCACGGAGCACAAGCCTGCACCTATCAAACATGTC
CCTGCAACCGACTCGGGAAAGAGTGCCCCCTGGACACAAGTCTCTGTACTGACACCAACTGT
GCCTCTCAGAGCACCAACCAGTACCAAGGACCACCACTACCCCTCCCCACCATCCACCTCAG
AAGCAGTCCCAGCCTGCCACCCGCCAGCCCCCTGCCAGCCCTGGTTGGAAACGGGTCA
GGATTGCCCTGGAGGATATTGGAATAGCCTCTTCAGTGTACAGAGATGCAACCAATA
GACAGAAACCAGAGG**TAA**TGCCACTTCATCCACATGAGGAGATGTCAGTATCTAACCTCT
CTGCCCTTCAATCCTAGCACCCACTAGATATTTAGTACAGAAAAACAAAATGGAAA
CACAA

FIGURE 214

MVPAAGALLWVLLNLGPRAAGAQGLTQTPTEMQRVSLRGPMTRSYRSTARTGLPRKTRI
ILEDENDAMADADRLAGPAAAELLAATVSTGFSRSSAINEEDGSSEEGVVINAGKDSTSREL
PSATPNTAGSSSTRFIANSQEPEIRLTSSLPRSPGRSTEDLPGSQATLSQWSTPGSTPSRWP
SPSPAMPSPEDLRLVLMPWGPWHCHCKSGTMSRSRGKLHGLSGRLRVGALSQLRTEHKPC
TYQQCPCNRLREECPLDTSLCDTNCASQSTTSTRTTTPFPTIHLRSSPSLPPASPCPALA
FWKRVVRIGLEDIWNSLSSVFTEMQPIDRNQR

FIGURE 215

CCCCGGTCAACCCACCGTCCGGGAGAAAGG**ATGGCCGGCTGGCGCGGTGGTCTGCTAGCTGGGCA**
GCGGCCTGGCGAGCGCTCCAGGGCACCCTGAGCCGGTACCGCAGCTCGTACTGCAGTGCAGAGACA
GAACCTGCTCTGGGGCGCTCTGAATCACTCCGCTCCGCCAGCCAATCTACATGAGTCTAGCAGGCTGGACCT
GTCGGGACGACTGTAAGTATGAGTGTATGGGTACCGTTGGCTCACCTCCAGGAAGGTACAAAGTGCT
CAGTTCCATGGCAAGTGGCCCTCTCCGGTCTCTGTTCTTCAGAGAGCCGCATCGGGCTGGCTCGTTCT
CAATGGCCTGGCCAGCCTGGTATGCTCTGCCGCTACCGCACCTCGTGCAGCCTCCCTCCCCCATGTACCA
CCTGTGTGCCCTCGCCTGGGTGTCCTCAATGCATGTTCTGGTCCACAGTCTTCCACACCAGGGACACTGAC
CTCACAGAGAAAATGGACTACTTCTGTGCCCTCACTGCATCCTACACTCAATCTACCTGTGCTGCCGTCAGGAC
CGTGGGCTGCAGCACCCAGCTGGTCAGTGCCTCCGGCTCTCGTGCATGCTGACCGTGCACGCT
CCTACCTGAGCCTCATCCGTTGACTATGGCTACAAACCTGGTGGCCAACCTGGTATGGCCTGGTCAACGTT
GTGTGGTGGCTGGCCTGGTGCCTGTTGGAACCCAGCGGGCTGCCTCACGTGCCAAGTGCCTGGTGGTGGT
GCTGTGCAGGGCTGTCCTGCTCGAGCTGCTGACTTCCCACCGCTCTCTGGGATGCCATGCCA
TCTGGCACATCAGCACCCATCCCTGTCACGCTCTTTCAGCTTCTGGAAAGATGACAGCCTGTACCTGCTG
AAGGAATCAGAGGACAAGTCAAGTCTGACTGA**AGACCTTGGAGCAGTCTGCCAGGGATCCTGCC**
GCCCTGCTGGCCTCCCTCTCCCCCTCAACCCCTGAGATGATTTCCTCTTCAACTTCTGAACTTGGACATGA
AGGATGTGGGCCAGAATCATGTGGCCAGCCCCCTGTTGGCCCTCACAGCCTGGAGCTGAACTGGGTGGAACGTGA
AAGGCCTCCCAGCATGGGACTGAGAGTGGCAGCCCCCTCACCTCCTGGAGCTGAACTGGGTGGAACGTGA
GTGTGTTCTAGCTTACCGGGAGGACAGCTGCCTGTTCTCCCCACCAGCCTCCTCCCCACATCCCCAGCTG
CCTGGCTGGGTCTGAAGCCCTGTCTACCTGGGAGACCAGGGACCACAGCCTTAGGGATACAGGGGGTCCC
CTTCTGTTACCAACCCCCACCCCTCCAGGACACCAACTAGGTGGTGTGGATGCTTGTCTTGGCCAGCAA
GGTTCACGGCATTCTCCCCATGGGATCTTGAGGGACCAAGCTGCTGGGATGGGAAGGAGTTCACCTGACC
GTTGCCCTAGCCAGGTCTCCAGGAGGCCTACCCATACTCCCTTCAGGGCAGGGCTCCAGCAAGCCAGGGCA
AGGATCCTGTGCTGCTGTTGGTGGAGACCTGCCACCGTGTGAGGAGTGTGGCCAGGCTGAGTGCATAGG
TGACAGGGCGTGGCATGGCTGGTCAAAAGTGTGTGTGCAAGGGGGTGGGTGTGTTAGCGTGGGTTAGGGAAACGTGTG
GGGGGAAGAGGTGTGGCTCAAAAGTGTGTGTGCAAGGGGGTGGGTGTGTTAGCGTGGGTTAGGGAAACGTGTG
TGCGCGTGTGGTGGCATGTGAGATGAGTGACTGCCGTGAATGTGTCACAGTTGAGGAGTTGGAGCAGGAT
GAGGGAACTCTGTCAACCATAATCACTTGAGGAGCCTGCCACCTGCCCAGACGCAACCTGGCGGACAGC
CAGGAGCTCTCCATGCCAGGCTGCCATGTGTCATGTTCCCTGTCGGTGCCTCTGGCCTCTGCAAAC
CTCACAGGGTCCCCACACAACAGTGCCTCCAGAACAGCAGCCCCCTGGAGGAGAGGAAGGAAAATGGGATGGC
TGGGGCTCTCCATCTCCCTTCTGCCATGCCATGGCTGGCTCCCTCCCAAAACCTCCATTCCCC
GCTGCCAGCCCCCTTGGCATAGCCGTGATTGGGGAGGGAGGAAGGGCGATTGAGGGAGAAGGGAGAAAGCT
TATGGCTGGGTCTGGTTCTCCCTCCAGAGGGTCTTACTGTTCCAGGGTGGCCCAGGGCAGGCAGGGGCC
ACACTATGCTGTGCCCTGGTAAGGTGACCCCTGCCATTACAGCAGCCCTGGCATGTTCTGCCCCCCACAGG
ATAGAAATGGAGGGAGCTCCAGAAAATTTCCATCCAAAGGCAGTCTCGTGGTTGAAGCAGACTGGATT
CTCTGCCCTGACCCCTTGTCCCTTTGAGGGAGGGAGCTATGCTAGGACTCCAAACCTCAGGGACTGGGTG
GCCTCGCCTAGCTCTTTGATACTGAAAATTTAAGGTGGGAGGGTGGCAAGGGATGTGCTTAATAATCAA
TTCCAAGCCTCAAAAAAAAAAAAAAA

FIGURE 216

MAGLAARLVLLAGAAALASGSQGDREPVYRDCVLQCEEQNCSGGALNHFRSRQPIYMSLAGW
TCRDDCKYECMWVTVGLYLQEGHKVPQFHGKWPFSRFLFFQE PASAVASFLNGLASLVMLCR
YRTFVPASSPMYHTCVAFAWVSLNAFWSTVFHTRDTDLTEKMDYFCASTVILHSIYLCCVR
TVGLQHPAVVSAFRALLLMLTVHVSYLSLIRFDYGYNLVANVAIGLVNVVWWLAWCLWNQR
RLPHVRKCVVVVLLLQGLSLELLDFPPLFWVLDHAIWHISTIPVHVLFFSFLEDDSLYLL
KESEDKFKLD

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domains:

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

N-glycosylation site.

amino acids 40-44

N-myristoylation site.

amino acids 43-49

CUB domain proteins profile.

amino acids 285-302

Amiloride-sensitive sodium channels proteins.

amino acids 162-186

FIGURE 217

FIGURE 218

MAPQSLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEFALTNEKSSTKETERKETKAEEEL
DAEVLEVFPHTHEWQALQPQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTN
TYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMV
RLINKFNSSSSSLEEKIAALFDLEYVHQMDNAQDLLSFGGLOVNINGLNSTEPLVKEYAAF
VLGAAFSSNPKVQVEAIEGGALQKLLVILATEQPLTAKKVLFALCSLLRHFPYAQRQFLKL
GGLQVLRTLQEKGTTEVLAVRVVTLLYDLVTEKMFAEEEAELTQEMSPEKLQQYRQVHLLPG
LWEQGWCEITAHLALPEHDAREKVLQTLGVLLTCRDRYRQDPQLGRTLASLQAEYQVLAS
LELQDGEGYFQELLGSVNSLLKELR

Important features:

Signal peptide:

amino acids 1-29

Hypothetical YJL126w/YLR351c/yhcX family protein.

amino acids 364-373

N-glycosylation site.

amino acids 193-197, 236-240

N-myristoylation site.

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

Homologous region SLS1 protein.

amino acids 68-340

FIGURE 219

TTCGGCTCCGTAGAGGAAGTGGCGCGGACCTTCATTGGGTTCGGTTCCCCCCTTCCC
 CTTCCCCGGGTCTGGGGTGACATGCACCGCGCCCTCGTGGGT CGCGTTGCCACCCCCA
 CGCGGACTCCCCAGCTGGCGGCCCTCCCATTGCCTGTCTGGTCAGGCCCCACCCCCC
 TTCCCACCTGACCAGCC**TGA**GGGCTGCGGTGTTTCGGCTGCACTTCGTCGGTCCGGC
 CGGGCCTCGCGCTTCTGATCACTGTGGCTGGGACCCGCTCGCGTTATCATCCTGGT
 CGCAGGGCATTTCCTGGCTGGTCCCTGCTCCTGGCTCTGTGGTCGGTTATCTGG
 TCCATGTGACCGACCGGTCAAGATGCCGGCTCCAGTACGGCCTCCTGATTTGGTGTGCT
 GTCTCTGCTTCTACAGGAGGTGTTCCGCTTGCCTACTACAAGCTGCTTAAGAAGGCAGA
 TGAAGGGTTAGCATCGCTGAGTGAGGACGGAAAGATCACCCATCTCCATCCGCAGATGGCCT
 ATGTTCTGGTCTCCTCGGTATCATCAGGGTGTCTCTGTTATCAATATTTGGCT
 GATGCACCTGGGCAGGTGTTGGGATCCATGGAGACTCACCTATTACTCCTGACTTC
 AGCCTTCTGACAGCAGCATTATCCTGCTCCATACCTTTGGGAGTTGTGTTCTTGATG
 CCTGTGAGAGGGAGACGGTACTGGCTTGGGCTGGTGGTTGGAGTCACCTACTGACATCG
 GGACTGACATTCTGAACCCCTGGTATGAGGCCAGCCTGCTGCCATCTATGCAGTCAGT
 TTCCATGGGCTCTGGCCTTCATCACAGCTGGAGGGTCCCTCGAAGTATTCAAGCGCAGCC
 TCTTGTGTAAGGAC**TGA**CTACCTGGACTGATGCCTGACAGATCCCACCTGCCTGTCCACTG
 CCCATGACTGAGCCCAGCCCCAGCCGGTCCATTGCCACATTCTGTCTCCTCTCGTC
 GGTCTACCCCACCTCCAGGGTTTGCTTGTCTTTGTGACCGTTAGTCTCTAAGCTT
 TACCAGGAGCAGCCTGGGTCAGCAGTCAGTGACTGGTGGGTTGAATCTGCACTATCCC
 CACCACCTGGGACCCCTGTTGTGTCAGGACTCCCCCTGTGTCAGTGCTCTGCTCTCAC
 CCTGCCAACACTCACCTCCCTCCCCCTGCAAGGCCAGGGAGGACAGTCGGGTGAT
 GGTGTATTCTGCCCTGCGCATCCCACCCGAGGACTGAGGGAACCTAGGGGGACCCCTGGC
 CTGGGTGCCCTCTGATGTCCTGCCCTGTATTCTCCATCTCAGTTCTGGACAGTGCAG
 GTTGCCAAGAAAAGGGACCTAGTTAGCCATTGCCCTGGAGATGAAATTAAATGGAGGCTCAA
 GGATAGATGAGCTCTGAGTTCTCAGTACTCCCTCAAGACTGGACATCTGGTCTTTCTC
 AGGCCTGAGGGGGAACCATTTGGTGTATAAATACCTAAACTGCCCTTTCTTTCTC
 GAGGTGGGGGGAGGGAGGGAGGTATATTGAAACTCTTCTAACCTCCTGGCTATATTCTC
 TCCTCGAGTTGCTCTCATGGCTGGCTCATTCGGTCCCTTCTGGTCCCAGACCTT
 GGGGAAAGGAAGGAAGTGCATGTTGGAACTGGCATTACTGGAACATAATGGTTAACCT
 CCTTAACCACCAAGCATCCCTCCTCCCCAAGGTGAAGTGGAGGGTGTGGTGAGCTGGC
 CACTCCAGAGCTGCAGTGCCACTGGAGGAGTCAGACTACCATGACATCGTAGGAAAGGAGGG
 GAGATTTTTGTAGTTTAATTGGGTGTTGGAGGGGGAGGTTTCTATAAAACTGT
 ATCATTCTGCTGAGGGTGGAGTGCCCATTAAATCAAGGTGATTGTGATTGACT
 AAAAAAAAGAATTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AAAAAAA

FIGURE 220

MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVIILVAGAFFWLVSLLASVVWFILVHVTDR
SDARLQYGLLIFGAAVSVLLQEVFRFAYYKLLKADEGLASLSLEDGRSPISIRQMAYVSGLS
FGIISGVFSVINILADALGPVGVGIHGDSPYYFLTSAFLTAIIILLHTFWGVVFIDACERRR
YWALGLVVGSLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQRSLLCKD

FIGURE 221

AAGCTGGTTAAGGAAGCAGAGGAGGGTAGATTGTTGAGTGAGGACGGAAGATCAACCCA
TTTCCATTCCGCCAGATGGCCTATGTTCTGGTCTCTCCCTCGGNATCATCAGTGGGTNT
TNTCTGTTATCAATATTTGGCTGATGCANTGGGCCAGGTGTGGTTGGGATCCATGGAGAC
TCACCCATTANTCCTGANTTCAGCCTTNTGACAGCAGCCATTATCCTGCTC

FIGURE 222

GACCGACCCTTCAGATGCCGGTCCAGTACGGCTCCTGATTGGTGCTGCTGTNTCTG
TCCTTCTACAGGAGGTGTTCCGCTTGCCTANTACAAGCTGCTTAAGAAGGCAGATGAGGGG
TTAGCATNGCTGAGTGAGGACGGAAGATCACCCATTCCATCCGCCAGATGGCCTATGTTN
TGGTNTTCCTTCGGTATCATCAGTGGTGTNTCTGTTATCAATATTTGGNTGATGCAN
TGGGCCAGGTGTGGTTGGGATCCATGGAGANTCACCTATTAAATTCCCTGAATTGCCTTT
NTGACAGCAGCCATTATCCTGNTCCATACCTTGGGGAGTTGTGTTTGATGCCTGTGA
GAGGAG

FIGURE 223

NGTTGGAGAAGTGGCGCGGACNTTCATTGGGTTTCGGTTCCCCCTTCCCTTCCCC
GGGTCTGGGTGACATTGCACGGGCCCTCGTGGGTCGCCTGCCACCCCACGCGGACTCC
CCAGNTGGNGGCCCTCCCATTGCCCTGCCTGGTCAGGCCCCACCCCCCTCCCACNTG
ACCAGCCATGGGGCTCGGGTGTTCGGCTGCACTTCGTCGCGTTCGGCCGGCCTCG
CGCTTTCTTGATCACTGTGGCTGGGACCCGTTCGCCTATCATCCTGGTCGAGGGCA
TTTTCTGGCTGGCTCCCTGCTCCTGGCCTCTGTGGTCTGGTCATCTGGCCATGTGAC
CGACCGGTCAAGATGCCGGCTCCAGTACGGCCTCCTGATTTGGTGCTGCTGTCTGTCC
TTCTACAGGAGGTGTTCCGCTTGCGCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGTTA
GCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTCTGG
TCTCTCCTTCGGTATCATCAGTGGTGTCTCTGTTATCAATATTTGGCTGATGCACTTG
GGCCAGGTGTGGTGGGATCCATGGAGACTCACCC

FIGURE 224

GTAAAAGAAAGTGGCCGGACCTCATTGGGGTTCGGTTCCCCCTTCCCNTCCCCGGGG
TCTGGGGGTGACATTGCACCGCGCCNTCGTGGGT CGCGTTGCCACCCCACGCGGACTCCC
CAGNTGGCGCGCCCTCCCATTGCCTGTCCTGGTCAGGCCCCACCCCCCTTCCCACCTGA
CCAGCCATGGGGCTGCGGTGTTTCGGGCTGCACTTCGT CGCGTT CGGGCCGGCCTTC
GCGCTTTCTTGATCACTGTGGCTGGGACCCGCTCGCGTTATCATCCTGGTCGCAGGGGC
ATTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTCATCTGGTCCATGTGA
CCGACC GGTCAGATGCCCGGCTCCAGTACGGCCTCCTGATTTGGTGCTGCTGTCTGTC
CTTCTACAGGAGGTGTTCCGCTTGCGCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGTT
AGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTCTG
GTCTCTCCTCGGTATCATCAGTGGTGTCTCTGTATCAATATTTGGCTGATGCACCT
GGGCCAGGTGTGGTTGGGATCCATGGAGAC

FIGURE 225

GCCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCGTGCCCAGAGCCCAGGAGGAGGCAG
 TGGCCAGGAAGGCACAGGCCTGAGAAGTCTGCGGCTGAGCTGGGAGCAAATCCCCCACCCCC
 TACCTGGGGACAGGGCAAGTGAGACCTGGTGAGGGTGGCTCAGCAGGCAGGGAAAGGAGAGG
 TGTCTGTGCGTCCTGCACCCACATCTTCTCTGTCCCCCTCCTGCCCTGTCTGGAGGCTGCT
 AGACTCCTATCTTCTGAATTCTATAGTGCCTGGGTCTCAGCGCAGTGCCGATGGTGGCCCGT
 CCTTGTGGTTCTCTACCTGGGAAATAAGGTGCAGCGGCC**ATG**GCTACAGCAAGACCCC
 CCTGGATGTGGGTGCTCTGTGCTCTGATCACAGCCTGCTTCTGGGGTCACAGAGCATGTT
 CTCGCCAACAAATGATGTTCTGTGACCACCCCTCTAACACCGTGCCCTCTGGGAGCAACCA
 GGACCTGGGAGCTGGGCCGGGAAGACGCCGGTCGGATGACAGCAGCAGGCCCATCATCA
 ATGGATCCGACTGCGATATGCACACCCAGCCGTGGCAGGCCGGCTGTTGCTAAGGCCAAC
 CAGCTCTACTGCAGGGCGGTGTTGGTGCATCCACAGTGGCTGCTCACGCCGCCACTGCAG
 GAAGAAAAGTTTCAGAGTCCGTCTCGGCCACTACTCCCTGTCACCAGTTATGAATCTGGG
 AGCAGATGTTCCAGGGGTCAAATCCATCCCCACCCCTGGCTACTCCCACCCCTGGCCACTCT
 AACGACCTCATGCTCATCAAACCTGAACAGAAGAATTGTCACAAAGATGTCAGACCCAT
 CAACGTCTCCTCTCATTGTCCTCTGCTGGACAAAGTGCTTGGTGTCTGGCTGGGGACAA
 CCAAGAGCCCCAAGTGCACCCCTAAGGTCCCTCCAGTGCTGAATATCAGCGTGCTAAGT
 CAGAAAAGGTGCGAGGATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCCGGTGA
 CAAAGCAGGTAGAGACTCCTGCCAGGGTGATTACCCCTGCCCCGCCAACAGACCGGGTGTAC
 TGCAGGGACTCGTGTCTGGGAGATTACCCCTGCCCCGCCAACAGACCGGGTGTAC
 ACGAACCTCTGCAAGTTACCAAGTGGATCCAGGAAACCATCCAGGCCACTCC**TGA**GTCAT
 CCCAGGACTCAGCACACCGGCATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTCAG
 ACCCTCATTCTCCAGAGATGTTGAGAATGTTCATCTCTCCAGGCCCTGACCCCATGTCT
 CCTGGACTCAGGGCTGCTTCCCCACATTGGGCTGACCGTGTCTCTAGTTGAACCCCTGG
 GAACAATTCCAAAATGTCAGGGGGGGTTGCGTCTCAATCTCCCTGGGGCACTTCAT
 CCTCAAGCTCAGGGCCCATCCCTCTGCAGCTGACCCAAATTAGTCCCAGAAATAAA
 CTGAGAAGTGGAAAAAA

FIGURE 226

MATARPPWMWVLCALITALLLGVTTEHVLANNVDSCDHPSNTVPSGSNQDLGAGAGEDARSDD
SSSRIINGSDCDMHTQPWQAALLLRPNQLYCGAVLVHPQWLTAHCRKKVFRVRLGHYSLS
PVYESGQQMFQGVKSIPHPGYSHPGHSNDLMLIKLNRRIRPTKDVRPINSSHCP SAGTKCL
VSGWGTTKSPQVHF PKVLQCLNISVLSQKR CEDAYPRQIDDTMFCAGDKAGR DSCQGDGGP
VVCNGSLQGLVSWG DYP CARPNR PGVYTNLCKFTKWIQETIQANS

FIGURE 227

ATGGTCAACGACC GG GTGG AAG ACC ATGGC GGC GCTGCCA ACTTGAGGACC GGCC GCG C
 CAAGCCGAGCGGCCGAGCTCGGCTACGTGCTGTGACCGTGCTGGCCCTGGCTGTGC
 TGCTGGCTGTAGCTGTCACCGGTGCCGTGCTTCTGAACCACGCCACGCCGGGCACG
 GCGCCCCCACCTGTCGTCAACTGGGCTGCCAGCGCCAACAGCGCCCTGGTCACTGTGGA
 AAGGGCGACAGCTCGCACCTCAGCATCCTCATGACCCGCGCTGCCCGACCTCACCGACA
 GCTTCGACGCCCTGGAGAGCGCCCAGGCCTCGGTGTCAGGGCCTGACAGAGCACCAGGCC
 CAGCCACGGCTGGTGGCGACCAGGAGCAGGAGCTGCTGGACACGCTGGCCGACCAGCTGCC
 CGGCTGCTGGCCGAGCCTCAGAGCTGCAAGACGGAGTGCATGGGCTGCGGAAGGGGCATG
 GCACGCTGGCCGAGGGCCTCAGGCCCTGCAAGACTGAGCAGGGCCTCATCCAGCTTCTC
 TCTGAGAGCCAGGGCACATGGCTCACCTGGTGAACCTCCGTCA CGACATCCTGGATGCCCT
 GCAGAGGGACC GG GG CTGGGCCGGCCCGAACAAAGGCCGACCTTCAGAGAGGCCCTGCC
 GGGGAACCCGGCCCGGGGCTGTGCCACTGGCTCCGCCCGAGACTGTCTGGACGTCTC
 CTAAGCGACAGCAGGACATGGCGTCACTCTGTCTTCCCACCCACTACCCGGCCGGCTT
 CCAGGTGACTGTGACATGCGCACGGACGGCGGCTGGACGGTGTTCAGCGCCGGAGG
 ACGGCTCGTGAACCTCTCCGGGGCTGGGACCGTACCGAGACGGCTTGGCAGGCTCACC
 GGGGAGCAGTGGCTAGGGCTCAAGAGGATCCACGCCCTGACCAACAGGCTGCCAACGAGCT
 GCACGTGGACCTGGAGGA CTTGAGAATGGCACGGCTATGCCGCTACGGGAGGCTTCGGCG
 TGGGCTTGTCTCGTGGACCCCTGAGGAAGACGGGTACCCGTCACCGTGGCTGACTATTCC
 GGCACGTGAGGCACTCCCTCGTGAAGCACAGCGGATGAGGTTCACCAAGGACCGTGA
 CAGCGACCAATTAGAGAACAAACTGTGCGCCCTTACCGCGGTGCGCACGCCCTCATGCCGACGGC
 GCCACACGCTCCAACCTCAATGGGAGTACCTGCGCGGTGCGCACGCCCTCATGCCGACGGC
 GTGGAGTGGTCTCTGGACCGGCTGGCAGTACTCAACTCAAGTCTGTGAGATGAAGATCCG
 GCCGGTCCGGAGGACCGCT**TAG**ACTGGTGCACCTTGTCTGGCCCTGCTGGTCCCTGTGCG
 CCCATCCCCGACCCACCTCACTTTCTGTGAATGTTCTCCACCCACCTGTGCCTGGCGGAC
 CCACTCTCCAGTAGGGAGGGCCGGCCATCCCTGACACGAAGCTCCCTGGGCCGGTGAAGT
 CACACATCGCCTCTCGCCGTCCCCACCCCTCATTGGCAGTCAGTACTGATCTTGCCTC
 TGCTGATGGGGCTGGCAA ACTTGACGACCCCAACTCCTGCCCTGCCCTACTGTGACTCCGG
 TGCTGTTGCCGTCCCTGCCAGGATGGTGGAGTCTGCCCTGCCAGGCACCCCTGCCCTGCC
 GGCCAAATACCGCATTATGGGACAGAGAGCAGGGGGCAGACAGCACCCCTGGAGTCTC
 CTAGCAGATCGTGGGAATGTCAAGGTCTCTGAGGTCTGAGGGCAGTATCCTCCAG
 CCCTCCCAATGCCAACCCCCACCCCGTTCTGTGCCCAGAGAAACCCACCTCTCCCCCAA
 GGGCCTCAGCCTGGCTGTGGCTGGGCCATCCCTACCGGCCCTGAGGTCAAGGATGGG
 GAGCTGCGCTTGGGACCCACGCTCCAAGGCTGAGACCAAGTCCCTGGAGGCCACCCAC
 CCTGTGCCCGGCAGGCCTGGGTCTGCA GTCTTACCTGCTGTGCCACCTGCTCTG
 TCTCAAATGAGGCCAACCCATCCCCACCCAGCTCCGGCGTCCTACCTGGGCAGC
 CGGGGCTGCCATCCATTCTCCTGCCCTGGAAGGTGGGTGGGCCCTGCACCGTGGGCT
 GGACTGCGCTAATGGGAAGCTCTGGTTTCTGGCTGGGCCCTAGGCAGGGCTGGGATGAG
 GCTTGTACAACCCCCACCAATTCTCCAGGGACTCCAGGGCTCTGAGGCCTCCAGGAGG
 GCCTTGGGGGTGATGACCCCTTCCCTGAGGTGGCTGTCCTCATGAGGAGGCCAACCCCTTGCC
 ATTGACCGTGGCACCTGGACCCAGGCCAGGGCCAGGCCAGGGGGCAGTGGTCAAGGGACAGGG
 CCACACTCACGGGCAAATGGGGCTGGGACCCAGGCCAGGGCCAGGCCAGGGCACCACCTGGACA
 CTTTCTTGTGAATCCTCCAACACCCAGCACGCTGTCA TCCCCACTCCTGTGTCACACA
 TGCA GAGGGTGA GAGACCCGCA GGCTCCAGGACCA GAGGCCACAAGGGCAGGGCTGGAGGCC
 TCCTCAGCTGTGCTCAGCAGCCCTGGACCCCGCGTGC GTTACGTCA GGCCAGATGCAGGG
 CGGCTTCTCAAGGCCTCTGATGGGGCTCCGAAAGGGCTGGAGTCAGCCTTGGGAGCT
 GCCTAGCAGCCTCTCCTGGGCA GGAGGGGAGGTGGCTTCCAAAGGACACCCGATGGCA
 GGTGCCTAGGGGGTGTGGGGTCCGTTCCCTCCACTGAAGTTGTGCTAAAA
 AACAAATAAATTGACTTGGCACCAGGTCA TCCACATGCGCAG
 TGTCCCAGTGCCACCAGGTCA TCCACATGCGCAG

FIGURE 228

MVNDRWKTMGAAQLEDRPRDKPQRPSCGYVLCTVLLALAVLLAVAVTGAVLFLNHAHAPGT
APPPVVSTGAASANSALVTVERADSSHLSILIDPRCPDLTDSFARLESAQASVLQALTEHQQA
QPRLVGDQEQUELLDTLADQLPRLLARASELQTECMGLRKGHGTLGQGLSALQSEQGR利QLL
SESQGHMAHLVNSVSDILDALQRDRGLGRPRNKADLQRAPARGTRPRGCATGSRPRDCLDVL
LSQQDDGVYSVFPTHYPAGFQVYCDMRTDGWTVFQRREDGSVNFFRGWDAYRDGFGRLT
GEHWLGLKRIHALTTQAAYELHVDLEDFENGAYARYGSFGVGLFSVDPEEDGYPLTVADYS
GTAGDSLLKHSGMRFTTKDRSDHSENNCAAFYRGAWWYRNCHTSNLNGQYLRGAHASYADG
VEWSSWTGWQYSLKFSEMKIRPVREDR

FIGURE 229

GCAGTCAGAGACTTCCCCTGCCCTCGCTGGAAAGAACATTAGGAATGCCTTTAGTGCCT
 TGCTTCCTGAACTAGCTCACAGTAGCCCGGCGGCCAGGGCAATCCGACCACATTCACTCT
 CACCGCTGTAGGAATCCAG**ATG**CAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATG
 ATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTGGCATCCAGAGCCC
 CGGCGCACAGAGCACAGGGCTCCCTTCAACGTGGCGACCAGTGGCCCTGACCCCTGCTGAC
 TTTGTGCTTGGTGCTGCTGATAAGGGCTGGCAGCCCTGGGCTTTGTTTCAGTACTACC
 AGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATACGTCC
 CAAGAGTTGCAATCTCTCAAGTCCAGAATATAAAGCTTGAGGAAGTCTGCAGCATGTGGC
 TGAAAAACTCTGCGTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTGTACAG
 ACAATGGAATGGCATGGAGACAATTGCTACCAAGTTCTATAAAGACAGCAAAAGTTGGGAG
 GACTGTAAATATTCTGCCTTAGTGAAAACCTCTACCATGCTGAAGATAAACAAACAAGAAGA
 CCTGGAATTGCGCGTCTCAGAGCTACTCTGAGTTTCTACTCTTATTGGACAGGGCTT
 TGCGCCCTGACAGTGGCAAGGCCTGGCTGGATGGATGGAACCCCTTCACTCTGAACTG
 TTCCATATTATAATAGATGTCACCAGCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGG
 GATGATCTTCTCAAAGGACTGCAAAGAATTGAAGCGTTGTCTGTGAGAGAAGGGCAGGAA
 TGGTGAAGCCAGAGAGGCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGAC**TGA**TTCGCC
 CTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTGAGACAT
 TGGGAAATGGAACATAATCAGGAAAGACTATCTCTGACTAGTACAAAATGGGTCTCGTG
 TTTCTGTTAGGATCACCAGCATTCTGAGCTGGGTTATGCACGTATTAACAGTCACA
 AGAAGTCTTATTACATGCCACCAACCAACCTCAGAAACCCATAATGTCATCTGCCTTCTG
 GCTTAGAGATAACTTTAGCTCTCTTCTCAATGTCTAATATCACCTCCCTGTTTCT
 GTCTCCTTACACTGGTGGAAATAAGAAACTTTGAAGTAGAGGAAATACATTGAGGTAAC
 ATCCTTTCTGACAGTCAAGTAGTCCATCAGAAATTGGCAGTCACTTCCCAGATTGTACC
 AGCAAATACACAAGGAATTCTTTGTTGTTCAGTCATACTAGTCCCTCCAAATCCAT
 CAGTAAAGACCCATCTGCCTTGTCCATGCCGTTCCAACAGGGATGTCACTGATATGAG
 AATCTCAAATCTCAATGCCTTATAAGCATTCTCCTGTGTCCATTAAGACTCTGATAATG
 TCTCCCTCCATAGGAATTCTCCAGGAAAGAAATATATCCCCATCTCGTTCATATCAG
 AACTACCGTCCCCGATATCCCTCAGAGAGATTAAGACCAGAAAAAGTGAGCCTCTCA
 TCTGCACCTGTAATAGTTCAGTCCTATTGACCCATATTACCTTCAG
 GTACTGAAGATTAAATAATAATGTAATAGTGTGAAAAA

230/330

FIGURE 230

MQAKYSSTRDMLDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCLVLL
IGLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRE
LYNKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAAS
QSYSEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIIDVTSPRSRDCVAILNGMIFSKD
CKELKRCVCERRAGMVKPESLHVPPETLGEGD

FIGURE 231

AATTTCACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGNTGG
ATGATGATGGGACACCACCATGAGCCTGCATTNTCAAGCTTTGCCACAATTGGCATCCAG
AGCCCCGGCGCACAGAGCACAGGNTCCTTTCAACGTGGCACCAGTGGCCCTGACCCTG
CTGACTTGTGCTGGTGCTGATAGGGCTGGCAGCCCTGGGCTTTGTTTCAGTA
CTACCAGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATA
CGTCCCAGAGTTGCAATTNTCAAGTCCAGAATATAAGCTTGCAGGAAGTNTGCAGCAT
GTGGCTGAAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGGAACCTTGAAGGAGGGCAA
AGTNCCATNTACTATACACACACCACTCCCC

FIGURE 232

CGCGAGCGCAAGAACCCCTGCGCAGCCCCAGAGCAGCTGCTGGAGGGGAATCGAGGCCGCGGCTC
CGGGGATT CGGCTCGGGCGCTGGCTCTGCTCTGCGGGGAGGGAGCGGGCCCGCGGGG
CCCGAGCCCCTCGGATCCGCCCCCTCCCCGGTCCCGCCCCCTCGGAGACTCCTCTGGCTGCT
CTGGGGGTT CGCCGGGGCGGGGACCCGCGGTCCGGCGCC **ATG** CGGGCATCGCTGCTGCTG
TCGGTCTCGGCCCCG CAGGGCCCGTGGCGTGGCATCTCCCTGGCTCACCTGAGCCT
GCTCAGCGTCACCTGGGTGGAGGAGCCGTGCGGCCAGGCCCGCCAAACCTGGAGACTCTG
AGCTGCCGCCGCCAACACCAACGCCGCGCCGGCCAACTCGGTGCAGCCCGAGCG
GAGCGCGAGAACGCCGGGGCGAAGGCCGGGGAGAAATTGGGAGCCGCGCTTGGCC
CTACCACCCCTGACAGGCCGCCAGGCCAAAAAGGCCGTAGGACCCGCTACATCAGCA
CGGAGCTGGCATCAGGAGGCTGCTGGTGGCGTGTGACCTCTCAGACACGCTGCC
ACGCTGGCGTGGCGTAACCGCACGCTGGGCAACCGGCTGGAGCGTGTGGTCTGAC
GGGCGACGGGCCGCCGGCCACCTGGCATGGCAGTGACGCTGGCGAGGAGCGAC
CCATTGGACACCTGCACCTGGCGTGCGCCACCTGCTGGAGCAGCACGGCAGCAGACTTGGAC
TGGTTCTCCTGGTGCCTGACACCACCTACACCGAGGCGCACGGCTGGCACGCC
CCACCTCAGCCTGGCCTCCGCCACCTGTACCTGGCCGGCCCCAGGACTTCATCGGC
GAGAGCCCACCCCCGGCGTACTGCCACGGAGGCTTGGGTGCTGTCGCGCATGCTG
CTGCAACAAC TGCCCCCACCTGGAGGCTGCCAACGACATCGTCACTGCGCGCCCTGA
CGAGTGGCTGGGTGCTGCATTCTCGATGCCACCAGGGTGGCTGACTGGTGACCACGAGG
GGGTGCACTATAGCCATCTGGAGCTGAGCCCTGGGAGCCAGTGCAAGGAGGGGAC
CTTCCGAAGTGCCCTGACAGCCCACCCCTGCGTGACCCCTGTGCACATGTAC
AGCTTCGCCCGAGCTGAACCTGGAAAGGCTGCCAACGACATCGTCACTGCGCGCC
TCCAGAATACCAGCCATCTGGCGTTGATGGGACCGGGCAGCTGCTGGCC
CCAGCACCATCCCGCCCTCCGCTTGAGGTGCTGCGTGGACTACTTCACGGAGCA
GCACGCTTCTCGGCCGATGGCTCACCCGCTGCCACTGCGTGGGCTGACCGGGCTG
ATGTGCCGATGTTCTGGGACAGCTTAGAGGAGCTGAACCGCCGCTACCACCGGGCTT
CGGCTCCAGAACGAGCAGCTGGTAATGGCTACCGACGCTTGATCCGGCCGGGTATGG
ATACACGCTGGACTTGCA GCTGGAGGCACTGACCCCCCAGGGAGGCCGGCC
GCCGAGTGCA GCTCCGGCGTGGAGGATCTGCTGTGCCCTATGTCACT
GAGGCCTCACGCTCACTGTGCTGCTGCCACTGCA GACTGGAGCTGGTGATGCT
CTTCTGGAGGCC TGTGCCACTGCA GACTGGAGCTGGTGATGCTGCGCAGCC
TGCTGCTACTGTATGAGCCGCGCAGGCCAGCGCTGGCCATGCA
GTCAAGGCCACGTGGCAGAGCTGGAGCGCTTCCCCTGGCTGCCATGGCTCAG
TGTGCAGACAGCCGCA CCTCACCAACTGCGCTCATGGATCTACTCTCAAGAAC
TGGACACACTGTTCTGCTGGCCGGCCAGACACGGTGCTCACGCTGACT
TGCCGCA TGCA TGCCATCTCGGCTGGCAGGCCCTTCCATGCA
CCCAGGTGTGGCCCCACACAAGGGCCTGGGCCAGAGCTGGCGTACACTGGCG
TTGATGCCAGGCAGCCAGCGAGGCTGCTCTACAAACTCCGACTAC
CGCCTGGCGGCA GCGCTCAGAACAGAACAGAGGAGCTGGAGAGCCTGG
GTTCCCTCACTCTCAGTCTGCA TGCGTGGGGCGTGGAGGCCGCTGCA
ACCGGGCCCAGACGTGCA GCGAGGCTCA GTGAGGACCTG TACCC
GTGCTTGAGGGCTCGGCTCCGAACCCAGCTGGCATGCTACT
CAACAGCACC **TGA** CCCACCCCTGCCCCGTGGCGTGGCATGGC
CTCCCCCAAACCAAGAGCCACCTGCCAGCCTCGCTGGCAGGGCTGGCGTAG
AAGCTGGCCCAC TGGTCCCTCTGGCTCTGTGGCTGGCTGG
GGACGTGCCAGGCCAGAGCCACCCACTTCTCATCCAAACCCAG
GTTGAGTCCAGTCTGCA TGCGTGGGGCGTGGAGGCCGCTGCA
ACCGGGCCCAGACGTGCA GCGAGGCTCA GTGAGGACCTG TACCC
GTGCTTGAGGGCTCGGCTCCGAACCCAGCTGGCATGCTACT
CAACAGCACC **TGA** CCCACCCCTGCCCCGTGGCGTGGCATGGC
CTCCCCCAAACCAAGAGCCACCTGCCAGCCTCGCTGGCAGGGCTGGCGTAG
AAGCTGGCCCAC TGGTCCCTCTGGCTCTGTGGCTGGCTGG
GGACGTGCCAGGCCAGAGCCACCCACTTCTCATCCAAACCCAG
GTTGAGTCCAGTCTGCA TGCGTGGGGCGTGGAGGCCGCTGCA
ACCGGGCCCAGACGTGCA GCGAGGCTCA GTGAGGACCTG TACCC
GTGCTTGAGGGCTCGGCTCCGAACCCAGCTGGCATGCTACT
CAACAGCACC **TGA** CCCACCCCTGCCCCGTGGCGTGGCATGGC
CTCTGGGCCCTGGGGCTGGCTGTAGAAGAGTTGGGGAGGGAGCTGAGGAGGG
GCATCTCCAAC TTCTCCCTTTGGACCCCTGCCAAGCTCC
AGTGTGGAAAAA

FIGURE 233

MRASLLSVLRPAGPVAVGISLGFTLSLLSVTWVEEPCGPQPGDSELPPRGNTNAARRP
NSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQAACKAVRTRYISTELGIRQRLLVAVL
TSQTTLPTLGVAVNRTLGHRLERVVFLTGARGRRAPPGMAVTLGEERPIGHLHIALRHLL
QHGDDFDWFFLVPDTTYTEAHGLARLTGHLSLASAAHLYLGRPQDFIGGEPTPGRYCHGGFG
VLLSRMLLQQLRPHELEGCRNDIVSARPDEWLGRCILDATVGVGCTGDHEGVHYSHLELSPGEPE
VQEGDPHFRSALTAHPVRDPVHMYQLHKAFARAEERTYQEIQELQWEIQNTSHLAVGDRA
AAWPVGIPAPSRRPASRFEVLRWDYFTEQHAFSCADGSPRCPLRGADRADVADVLGTALEELN
RRYHPALRLQKQQLVNGYRRFPARGMEYTLDLQLEALTPOGGRRPLTRRVQLLRPLSRVEI
LPV PVY VTE ASR LTV LL PLAAA E RD LAP G FLE A FATA A LE PG DAAA AL T L L L Y E PR Q A QR VA
HAD VF AP V KAH VAE LERR F P G A R V P W L S V Q T A A P S P L R I M D L L S K K H P L D T L F L L A G P D T V L
TPDFLNRCRMHAISGWQAFFPMHFQAFHPGVAPPQGPGPPELGRDTGRFDRQAASEACFYNS
DYVAARGRLAAASEQEEELLESLDVYELFLHFSSLHVLRAVEPALLQRYRAQTCSARLSEDL
YHRCLQSVLEGLGSRTQLAMLLFEQEQGNST

FIGURE 234

GCTCTGGCCGGCCCCGGCGATTGGTCACCGCCCGTAGGGGACAGCCCTGGCCTCCTCTGAT
 TGGCAAGCGCTGGCACCTCCCCACACCCCTGCGAACGCTCCCTAGTGGAGAAAAGGAGT
 AGCTATTAGCCAATTGGCAGGGCCCCTTTAGAAGCTTGATTTCCTTGAAGATGAAAG
 ACTAGCGGAAGCTCTGCCTCTTCCCCAGTGGCGAGGGAACTCGGGCGATTGGCTGGAA
 CTGTATCCACCAAATGTCACCGATTCTCCTATGCAGGAAATGAGCAGACCCATCAATAA
 GAAATTCTCAGCCTGGCCAAAATGGTGGCCCCACGAAGCCACGACAACGGAGGCAAAG
 AGGGTTGCTCAACGCCCGCCTCATGGAAAACCAAATCAGATCTGGACCTATAGCGTG
 GCGGAGGGGGCGATGATTGTCGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCTTCT
 TTCCCCGCCCTGAGACCCTGCAGCACCATCTGTC**ATG**GC GGCTGGCTGTTGGTTGAGC
 GCTCGCGTCTTGGCGCAGCGCGACCGAGGGCTCCGGCCGCCGTCCGCTGGGA
 ATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCGCTGTGGCGGGAAAGCGGCCCCCAGAAC
 CGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGACGAAAACCTGTATGAGAAGAACCA
 GACTCCCAGGTTATGACAAGGACCCGTTTGGACGTCTGGAACATGCGACTTGTCTTCTT
 CTTGGCGTCTCCATCATCCTGGCCTTGGCAGCACCTTGTGGCTATCTGCCTGACTACA
 GGATGAAAGAGTGGTCCCGCCGGAAGCTGAGAGGCTTGTGAAATACCGAGAGGCCAATGGC
 CTTCCCATCATGGAATCCAAGTGGGCTCAAGAAGCACCCTCCACCCCTGCCATTCTGAC
TG
ACCAGTTGCTAAGTGGGCTCAAGAAGCACCCTCCACCCCTGCCATTCTGAC
 CTCTCTCAGAGCACCTAATTAAAGGGCTGAAAGTCTGAA

FIGURE 235

MAAGLFGLSARRLLAAAATRGLPAARVRWESSFSRTVVAPS A VAGKRPPEPTTPWQEDPEPE
DENLYEKNPDSHGYDKDPVLDVWNMRLVFFFGVSIILVLGSTFVAYLPDYRMKEWSRREAER
LVKYREANGLPIMESNCFDPSKIQLPEDE

FIGURE 236

GGCGGGCTGGGCTGTTGGTTGAGCGCTGCCGTCTTGGCGCAGCGCGACGCGAGGGC
TCCCGGCCGCCCGCGTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCT
GTGGCGGGAAAGCGGCCCGAGAACCGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGA
CGAAAACTTGTATGAGAAGAACCCAGACTCCCATGGTTATGACAAGGACCCGTTGGACG
TCTGGAACATGCGACTTGTCTTCTTGGCGTCTCCATCATCCTGGTCCTGGCAGCACC
TTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCGCCGGAAGCTGAGAGGCT
TGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAAGTGCCTCGACCCAGCA
AGATCCAG

FIGURE 237

GCGGGGGCT**ATG**CCGCTTGCCTGCTCGTCTGGGCCCCGGCGGCTGGTGCCT
 TGCAGAACCCCCACGCGACAGCCTGCGGGAGGAACCTTGTCATCACCCCGCTGCCTCCGGGG
 ACGTAGCCGCCACATTCCAGTTCCGCACGCCTGGGATTGGAGCTTCAGCGGGAAAGGAGTG
 TCCCATTACAGGCCTTTCCAAAGCCCTGGGGCAGCTGATCTCAAGTATTCTACGGGA
 GCTGCACCTGTCAATTACACAAGGCTTGGAGGACCCGATACTGGGGGCCACCCTCCTGC
 AGGCCCATCAGGTGCAGAGCTGTGGTCTGGTCAAAGACACTGTCACTGATGTGGATAAA
 TCTTGGAAAGGAGCTAGTAATGTCCTCAGGGATCTCTGCGCCTCTCAACTTCATCGA
 CTCCACCAACACAGTCACTCCACTGCCTCCTCAAACCCCTGGGTCTGGCAATGACACTG
 ACCACTACTTCTGCCTATGCTGTGCTGCCGCGGGAGGTGGTCTGCACCGAAAACCTCACC
 CCCTGGAAGAAGCTTGCCTGTAGTCCAAGGCAGGCCTCTGTGCTGCTGAAGGCAGA
 TCGCTTGTCCACACCAGCTACCACTCCAGGCAGTGCATATCGCCCTGTTGCAGAAATG
 CACGCTGTACTAGCATCTCCTGGGAGCTGAGGCAGACCCCTGTCAAGTTGATTCGCTTC
 ATCACGGGCAGGAAAGAAAGACTGGTCCCTCTCCGGATGTTCTCCGAACCCCTCACGGA
 GCCCTGCCCTGGCTCAGAGAGCCGAGTCTATGTGGACATCACCACCTACAACCAGGACA
 ACGAGACATTAGAGGTGCACCCACCCCGACCACATACATCAGGACGTACCTAGGCACT
 CGGAAGACCTATGCCATCTATGACTGCTTGACACCGCCATGATCAACAACCTCTGAAACCT
 CAACATCCAGCTCAAGTGGAAAGAGACCCCCAGAGAATGAGGCCCCCAGTGCCTTC
 ATGCCAGCGGTACGTGAGTGGCTATGGGCTGAGAAGGGGGAGCTGAGCACACTGCTGTAC
 AACACCCACCCATACCGGGCTTCCCGGTGCTGCTGGACACCGTACCTGGTATCTGCG
 GCTGTATGTGCACACCCTACCATCACCTCCAAGGGCAAGGAGAACAAACCAAGTTACATCC
 ACTACCAGCCTGCCAGGACCGGCTGCAACCCACCTCTGGAGATGCTGATTAGCTGCCG
 GCCAACTCAGTCACCAAGGTTCCATCCAGTTGAGCGGGCGCTGCTGAAGTGGACCGAGTA
 CACGCCAGATCTAACCATGGCTCTATGTCAGCCCCTGTCCCTAGCGCCCTTGTGCCCA
 GCATGGTAGCAGCCAAGCCAGTGGACTGGGAAGAGAGTCCCCTTCAACAGCCTGTTCCA
 GTCTCTGATGGCTCTAACATACCTTGTCGGCTCTACACGGAGCCGCTGCTGGTAAACCTGCC
 GACACCGGACTTCAGCATGCCCTACACGTGATCTGCCCTACGTGCACTGTGGTGGCCGTG
 GCTACGGCTCCTCTACAATCTCCTCACCGAACCTCCACATCGAGGAGCCCCCACAGGT
 GGCCTGGCCAAGCGGCTGGCAACCTTATCCGGCGCGCCCGAGGTGTCCCCCCTACT**TGA**TT
 CTTGCCCTTCCAGCAGCTGCAGCTGCCGTTCTCTCTGGGAGGGAGCCAAGGGCTGTT
 TCTGCCACTTGCTCTCCTCAGAGTTGGCTTTGAACCAAAGTGCCTGGACAGGTCAAGGGC
 CTACAGCTGTGTTCCAGTACAGGAGCCACGAGCCAAATGTGGCATTGAATTGAATTAA
 CTTAGAAATTCAATTCTCACCTGTAGTGGCACCTCTATATTGAGGTGCTCAATAAGCAA
 AGTGGTCGGTGGCTGTTGACAGCAGAAAAAGATTCCATCACCACAGAAAGGTC
 GGCTGGCAGCACTGGCCAAGGTGATGGGTGTGCTACACAGTGTATGCACTGTGAGTGG
 TGGAGTTACTGTTGTGGAATAAAACGGCTGTTCCGTGGAAAAAAAAAAAAA

FIGURE 238

MPLALLVLLLLGPGGWCLAEPPRDSLREELVITPLPSGDVAATFQFRTRWDSELQREGVSHY
RLFPKALGQLISKYSLRELHLSFTQGFWRTRYWGPPFLQAPSGAELWVWFQDTVTDVDKSWK
ELSNVLSGIFCASLNFDSTNTVTPTASFKPLGLANDTDHYFLRYAVLPREVVCTENLTPWK
KLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCRNARCTSISWELRQTLSVVFDAFITG
QGKKDWSLFRMFSRTLTEPCPLASESRVYVDITTYNQDNETLEVHPPPTTYQDVILGTRKT
YAIYDLLDTAMINNSRNLNQIQLKWKRPENEAPPVPFLHAQRYSGYGLQKGELSTLLYNTH
PYRAFPVLLLDTVPWYLRLYVHTLTITSKGKENKPSYIHYQPAQDRLQPHLLEMLIQLPANS
VTKVSIQFERALLKWTEYTPDPNHGFYVSPSVLSALVPSMVAAKPVDWEESPLFNSLFPVSD
GSNYFVRLYTEPLLVLNLPDFSMPYNVICLTCTVVAVCYGSFYNLLTRTFHIEEPRTGGLA
KRLANLIRRARGVPPL

FIGURE 239

CAACATGGGGTCCAGCAGCTTCTGGTCCTCATGGTGTCTCGTTCTTGTGACCCTGGTGG
CTGTGGAAGGAGTTAAAGAGGGTATAGAGAAAGCAGGGGTTGCCAGCTGACAACGTACGC
TGCTTCAAGTCCGATCCTCCCCAGTGTACACAGACCAGGACTGTCTGGGGAAAGGAAGTG
TTGTTACCTGCACTGTGGCTTCAAGTGTGATTCTGTGAAGGAACTGGAAGAAGGAGGAA
ACAAGGATGAAGATGTGTCAAGGCCATACCCCTGAGCCAGGATGGGAGGCCAAGTGTCCAGGC
TCCTCCTCTACCAGGTGTCTCAGAAATGATGCTGGGCCTTCTACCTCTGGGGTCACTC
TCACTTGGCACCTGCCCTGAGGGCCTGAGACTTGAAGTCTTCCCCAAAAGAGGGAAAGAGTCACAAAAAG
TCCAGACCCCAGGGACGGTACTTCCCTCTACCTGGTGCCTCCCTAATGCTCATGAAT
GGACCCCTCATGAATGAAACCAGTGCCCTATAAGAGACCCAAAGAGCTGCCTGCCCTTC
TGCAATGTGTGATCACAGCTAGAAGGCAGTGTCAAGAGAGAAACTGGCCTCACCAAGATG
CTGAATCTGCTGGTGCCTGATCTGGACTTCCCAGCCTCTAGAACTGTAAGAAATAATAT
TTGCTGTTATAATCCAA

FIGURE 240

MGSSSFLVLMVSLVLVTLVAVEGVKEGIEKAGVCPADNVRCFKSDPPQCHTDQDCLGERKCC
YLHCGFKCVIPVKELEEGGNKDEDVSRPYPEPGWEAKCPGSSSTRCPQK

Signal sequence:

amino acids 1-19

N-myristoylation sites:

amino acids 23-29, 27-33, 32-38, 102-108

WAP-type 'four-disulfide core' domain signature:

amino acids 49-63

FIGURE 241

AAACCTCAGCACTGCCGGAGTGGCTCATTGTTAAGACAAAGGGTGTGCACTTCCCTGGCCAGG
 AAACCTGAGCGGTGAGACTCCCAGCTGCCTACATCAAGGCCCAAGGACATGCAGAACCTTCC
 TCTAGAACCCGACCCACCACCA**TG**AGGTCCTGCCTGTGGAGATGCAGGCACCTGAGCCAAGG
 CGTCCAGTGGCCTTGCTTCTGGCTGTGGTCTTCTTCTTCGCCTGCCCTTTTA
 TTAAGGAGCCTCAAACAAAGCCTTCCAGGCATCAACGCACAGAGAACATTAAGAAAGGTCT
 CTACAGTCCCTGGCAAAGCCTAAGTCCAGGCACCCACAAGGGCAGGGAGGACAACCATCTA
 TGCAGAGGCCAGCGCCAGAGAACATGCCCTCAACACACAAACCCAGGCCAAGGCCACACCA
 CCGGAGACAGAGGAAAGGAGGCCAACCGGACCGCCGGAGGAGCAGGACAAGGTGCCAC
 ACAGCACAGAGGGCAGCATGGAAGAGCCCAGAAAAAGAGAAAACCATGGTGAACACACTGTC
 ACCCAGAGGGCAAGATGCAGGGATGGCCTCTGGCAGGACAGAGGCACAATCATGGAAGAGCC
 AGGACACAAAGACGACCAAGGAAATGGGGGCCAGACCAGGAAGCTGACGGCCTCCAGGACG
 GTGTAGAGAAGCACCAGGGCAAAGCGGCAACCACAGCCAAGACGCTCATCCCCAAAGTCA
 GCACAGAATGCTGGCTCCACAGGAGCAGTGTCAACAAGGACGAGACAGAAAGGAGTGACCA
 CAGCAGTCATCCCACCTAAGGAGAACCTCAGGCCACCCACCCCTGCCCTTCCAG
 AGCCCCACGACGAGAACAAAGACTGAAGGCCAACCTCAAATCTGAGCCTCGGTG
 GGATTTGAGGAAAAATACAGCTCGAAATAGGAGGCCTCAGACGACTTGCCTGACTCTG
 TGAAGATCAAAGCCTCCAAGTCGCTGTGGCTCCAGAAACTCTTCTGCCAACCTCACTCTC
 TTCCTGGACTCCAGACACTCAACCAAGACTGAGTGGGACCGCCTGGAACACTTGCACCACC
 CTTGGCTTCATGGAGCTCAACTACTCCTTGGTGCAGAAGGTGCTGACACGCTCCCTCCAG
 TGCCCCAGCAGCTGCTCCGGCCAGCCTCCCCGCTGGAGCCTCCGGTGCATCACCTGT
 GCCGTGGGGCAACGGGGCATCCTGAACAACTCCCACATGGCCAGGAGATAGACAGTCA
 CGACTACGTGTTCCGATTGAGCGGAGCTCTCATTAAAGGCTACGAACAGGATGTGGGACTC
 GGACATCCTCTACGGCTTACCGCCTCTCCCTGACCCAGTCACTCCTATATTGGGCAAT
 CGGGGTTCAAGAACGTGCTCTGGGAAGGACGTCCGCTACTGCACTCCTGGAAAGGCAC
 CCGGGACTATGAGTGGCTGGAAGCAGTGTATGAATCAGACGGTATGTCAAAAAACCTT
 TCTGGTTAGGCACAGACCCAGGAAGCTTTCGGGAAGGCCCTGCACATGGACAGGTACCTG
 TTGCTGCACCCAGACTTCTCGATACATGAAGAACAGGTTCTGAGGTCTAAGACCCCTGGA
 TGGTGCCACTGGAGGATATACGCCCAACTGGGCCCTCCTGCTGCTCACTGCCCTTC
 AGCTCTGTGACCAGGTGAGTGTATGGCTCATCACTGAGGCCATGAGCGCTTCTGAT
 CACTACTATGATAACATCATGGAAGCGGCTGATCTTACATAAACCATGACTTCAAGCTGGA
 GAGAGAAGTCTGGAAGCGGCTACACGATGAAGGGATAATCCGGCTGTACCAGCGTCTGGTC
 CCGGAACTGCCAAGCCAAG**TG**ACCGGGCCAGGGCTGCCATGGTCTCCTGCTGCTC
 CAAGGCACAGGATACAGTGGAAATCTTGAGACTCTTGGCATTCCATGGCTCAGACTAA
 GCTCCAAGCCCTCAGGAGTCCAAGGGAACACTGAAACCAGGACAAGACTCTCAAGAT
 GGCAAATGGCTAATTGAGGTTCTGAAGTTCTCAGTACATTGCTGTAGGTCTGGCCAGG
 GATTTTAATTAAATGGGGTATGGGTGGCCAATACCACAATTCTGCTGAAAAACACTTT
 CCAGTCCAAAAGCTTCTTGATACAGAAAAAGAGCCTGGATTACAGAAACATATAGATCTG
 GTTGAAATTCCAGATCGAGTTACAGTGTGAAATCTGAGGTATTACTTAACCTCACTAC
 AGATTGTCTAGAAGACCTTCTAGGAGTTATCTGATTCTAGAAGGGTCTATACTTGCTTGT
 TCTTTAAGCTATTGACAACCTACAGTGTGTTAGAAAATGATAATAACAAATGATTGTT
 GTCCATGGAAAGGCAAATAAATTCTACAGTGAaaaaaaaaaaaaaa

FIGURE 242

MRSCLWRCRHLSQGVQWSLLLAVLVFFLFALPSFIKEPQT KPSRH QRTENIKERSLQLSLAKP
KSQAPTRARRTTIYAE PAPENN ALNTQTPKAHTTGDRGKEANQAPPEE QDKVPH TAQRAAW
KSPEKEKTMVN T LSPRGQDAGMASGRTEAQSWKSQDTKTTQGNNGQTRKL TASRTVSEKHQG
KAATTAKTLIPKSQH RMLAP TGAVSTRTRQKG VTTAVIPPKEKKPQATPPPAPFQSPTTQRN
QRLKAANFKSEPRWD FEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKLFLPNLTFLDSRHF
NQSEWDRLEHFAPPFGFMELNYSLVQKV VTRFP PV PQQQ LLLASLPAGSLRCITCAVVGNGG
ILNNNSHMQEIDSHDYVFR LSGALIKGYEQDVGTRTSFYGFTAFSLTQSLLILGNRGFKNVP
LGKDVRYLHFLEGTRDYEWLEALLMNQTVMSKNLFWFRHRPQEAFREALHMDRYLLLHPDFL
RYMKNRFLRSKTLDGAHWRIYRPTTGALLLTALLCDQVSAYGFITEGHERFS DHYY DTSW
KRLIFYINHDFKL EREVWKRLHDEGIIRLYQRPGPGTAKAKN

Cytoplasmic Domain:

amino acids 1-10

Type II Transmembrane Domain:

amino acids 11-35

Lumenal catalytic Domain:

amino acids 36-600

Ribonucleotide Reductase small subunit Signature:

amino acids 481-496

N-glycosylation Sites:

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

FIGURE 243

CGATGCGCGACCCGGCACCCCTCCTGGGCTGCTGGTGTGGGCCTCGCCG
GAGCAGCGAGTGGAAATTGTCCTCGAGATCTGAGGATGAAGGACAAGTTCTAAAACACCT
TACAGGCCCTTTTATTTAGTCAAAGTGCAGCAAACACTCCATAGACTTATCACAACA
CCAGAGACTGCACCATTCCGCATACTATAAAAGATGCGCCAGGCTTACCCGGCTGGCT
GTCAGTCCAGTGTGCATGGAGGATAAGTGAGCAGACCGTACAGGAGCAGCACACCAGGAGCC
ATGAGAAGTGCCTGGAAACCAACAGGGAAACAGAACTATCTTATACACATCCCCTCATGG
ACAAGAGATTTATTTGCAGACAGACTCTCCATAAGTCCTTGAGTTGTATGTTGTTG
ACAGTTGCAGATATATTCGATAAATCAGTGTACTGACAGTGTATCTGTCACTTATT

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FIGURE 244

MRGPGHPLLGLLLVLGPSPEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNT
RDCTIPAYYKRCARLLTRLAVSPVCMEDK

FIGURE 245

GGGCTGGGCCCGCCGCAGCTCCAGCTGGCCGGCTTGGTCTGCGGTCCCTCTCTGGGAGG
CCCGACCCCGGCCGCCAGCCCCACCATGCCACCCGCCGGCTCCGCCGGGCCGCCG
CTCACCGCAATCGCTCTGTTGGTCTGGGCTCCCTGGTCTGGCCGGCGAGGACTGCCT
GTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGTTAACTGCGAGTTCTCACCTCT
GCTGCCGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTGCTTATCACCGAGAGG
CAGCAGAAGCACTGCCTGCCCTCAGCCCCAAGACCATAGCAGGCATGCCTCAGCTGTGAT
CCTCTTGTGCTGTGGTGCACCACCATCTGCTGCTTCCTCTGTTCTGCTACCTGT
ACCGCCGGCGCCAGCAGCTCCAGAGCCCATTGAAGGCCAGGAGATTCCAATGACAGGCATC
CCAGTGCAGCCAGTATAACCCATACCCCCAGGACCCCAAAGCTGCCCTGCACCCCCACAGCC
TGGCTTCATGTACCCACCTAGTGGTCTGCTCCCAATATCCACTCTACCCAGCTGGGCC
CAGTCTACAACCCCTGCAGCTCCTCCCTATATGCCACCACAGCCCTTACCCGGGAGCC
TGAGGAAACCAAGCCATGTCTTGCTGCCCTTCAGTGATGCCAACCTGGGAGATGCCCTCAT
CCTGTACCTGCATCTGGTCTGGGGTGGCAGGAGTCCTCCAGCCACCAGGCCAGACCAA
GCCAAGCCCTGGGCCCTACTGGGACAGAGCCCCAGGGAAGTGGAACAGGAGCTGAACAG
ACTATGAGGGTTGGGGGAGGGCTTGAATTATGGGCTATTTACTGGGGCAAGGGAGG
GAGATGACAGCCTGGTCACAGTGCCTGTTCAAATAGTCCCTTGCTCCCAAGATCCCAG
CCAGGAAGGCTGGGCCCTACTGTTGTCCCCCTGGCTGGGTGGGGGAGGGAGGAGGT
TCCGTCAGCAGCTGGCAGTAGCCCTCCTCTGGCTGCCCACTGGCACATCTGGCCTG
CTAGATTAAAGCTGTAAAGACAAAA

FIGURE 246

MPPAGLRRAAPLTAIALLVLGAPLVLAGEDCLWYLDRNGSWHPGFNCEFFTFC
CRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICFLCSCCYLYRRRQQLQSP
FEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYNPAAPPP
YMPPQPSYPGA

Transmembrane Domains:

amino acids 10-28, 85-110

N-glycosylation Site:

amino acids 38-41

N-myristoylation Sites:

amino acids 5-10, 88-93

FIGURE 247

GGGGGAGCTAGGCCGGCGGAGTGGGGTGGCGGGCGCAAGGGTGAGGGCGGGCCCCAGAA
 CCCCAGGTAGGTAGAGCAAGAAG**ATG**GTGTTCTGCCCTCAAATGGTCCCTTGCAACCAG
 TCATTTCTACTTTCTCACTGTTGGCTCTTAACGTGTCACCTCCTCATGGTGTGAG
 CACTGAAGCATCTCCAAAACGTAGTGTAGGGACACCATTCTGGAATAAAATACGACTTC
 CTGAGTACGTACCTCCAGTCATTATGATCTTGATCCATGCAAACCTTACACGCTGACC
 TTCTGGGAACACAGAAGTAGAAATCACAGCCAGTCAGGCCACCCAGCACCACATCCTGCA
 TAGTCACACCTGCAGATATCTAGGGCCACCCCTCAGGAAGGGAGCTGGAGAGAGGGCTATCGG
 AAGAACCCCTGAGGTCTGGAACACCCCCCTCAGGAAGGGAGCTGGAGAGAGGGCTATCGG
 CCCCTCTGTGGCTCCGTACACAGTTGTCATTCACTATGCTGGCAATCTTCGGAGAC
 TTCCACGGATTACAAAAGCACCTACAGAACCAAGGAAGGGAACTGAGGAACTAGCAT
 CAACACAATTGAAACCCACTGCAGCTAGAATGGCTTCCCTGCTTGATGAACCTGCCTTC
 AAAGCAAGTTCTCAATCAAATTAGAAGAGAGCCAAGGCACCTAGCCATCTCAAATGCC
 ATTGGTGAATCTGTGACTGTTGCTGAAGGACTCATAGAACGACATTGATGTACTGTGA
 AGATGAGCACCTATCTGGTGGCCTCATCATTACAGATTGAGTCTGTCAGCAAGATAACC
 AAGAGTGGAGTCAGGTTCTGTTATGCTGTGCCAGACAAGATAATCAAGCAGATTATGC
 ACTGGATGCTGCGGTGACTCTCTAGAATTATGAGGATTATTCAGCATAACCGTATCCCC
 TACCCAAACAAGATCTGCTGCTATTCCGACTTTCAGTCTGGTCTATGGAAAAGTGGGG
 CTGACAAACATATAGAGAACCTGCTCTGTTGATGCAGAAAAGTCTCTGCATCAAGTAA
 GCTTGGCATCACAGTGAATGTTGCTGGCCATGAACCTGGCCACCGTGGTTGGAACCTGGTCA
 CTATGGAATGGTGAATGATCTTGGCTAAATGAAGGATTGCTTGGCAAATTATGGAGTTGTG
 TCTGTCAGTGTGACCCATCCTGAACGAAAGTTGGAGATTATTCTTGGCAAATGTTG
 CGCAATGGAGGTAGATGCTTAAATCCTCACACCCCTGTCACACCTGTGAAAATCCTG
 CTCAGATCCGGAGATGTTGATGATGTTCTTATGATAAGGGAGCTGTATTCTGAATATG
 CTAAGGGAGTATCTTAGCGCTGACGCATTAAAAGTGGTATTGTACAGTATCTCCAGAAC
 TAGCTATAAAAATACAAAAACGAGGACCTGTGGTAGTATGGCAAGTATTGCCCTACAG
 ATGGTGTAAAAGGGATGGATGGCTTGCTAGAACATTACATCTCATCCTCACAT
 TGGCATCAGGAAGGGTGGATGTGAAAACCATGATGAACACTTGGACACTGCAGAGGGTT
 TCCCCTAATAACCATCACAGTGAGGGGGAGGAATGTACACATGAAGAACAGACTACATGA
 AGGGCTCTGACGGCGCCCCGGACACTGGTACCTGTGGCATGTTCCATTGACATTCATCACC
 AGCAATCCAACATGGTCCATCGATTGGCTTAAACAAAGATGGTATTACATTGTGCAATTACG
 AGAAGAGGTGGAATGGATCAAATTAAATGTGGCATGAATGGCTATTACATTGTGCAATTACG
 AGGATGATGGATGGACTCTTGACTGGCTTTAAAGGAACACACAGCAGTCAGCAGT
 ATGATGGCAAGTCTCATTAACAAATGCATTTCAGCTCGTCAGCATTGGGAAGCTGTCCAT
 TGAAAAGGCCTGGATTATCCCTGACTTGAAACATGAAACTGAAATTATGCCGTGTT
 AAGGTTGAATGAGCTGATTCTATGTATAAGTTAATGGAGAAAAGAGATATGAATGAAGTG
 GAAACTCAATTCAAGGCCTCCTCATCAGGCTGCTAAGGGACCTCATTGATAAGCAGACATG
 GACAGACGAGGGCTCAGTCAGAGCAAATGCTGCGGAGTGAACACTACTCCTCGCCTGTG
 TGCACAACATCAGCCGTGCGTACAGAGGGCAGAAGGCTATTGAGAAAGTGGAGGAATCC
 AATGGAAACTTGAGCCTGCTGACGTGACCTGGCAGTGTGGCTGGGGCCAGAG
 CACAGAAGGCTGGATTCTTATAGTAAATATCAGGTTCTTGTGCTTGGCTACTGAGAAAA
 GCCAAATTGAATTGCCCCTGCGAGAACCCAAAATAAGGAAAGCTCAATGGCTACTAGAT
 GAAAGCTTAAGGGAGATAAAATAAAACTCAGGAGTTCCACAAATTCTTACACTCATGG
 CAGGAACCCAGTAGGATACCCACTGGCCTGGCAATTCTGAGGAAAACGGAAACAAACTTG
 TACAAAAGTTGAACCTGGCTCATCTCCATAGGCCACATGGTAATGGGTACAACAAATCAA
 TTCTCCACAAGAACACGGCTTGAAGAGGTTAAAGGATTCTCAGCTCTTGAAAGAAAATGG
 TTCTCAGCTCCGGTGTGTCACAGACAATTGAAACCATTTGAAAGAAAACATCGGTTGGATGG
 ATAAGAATTGATAAAATCAGAGTGTGGCTGCAAAGTGAAGGGCTTGAACGTATG**TAAAAA**
 TTCCTCCCTGCCCCGGTCTGTTATCTCTAATCACCAACATTGTTGAGTGTATTGAA
 ACTAGAGATGGCTGTTGGCTCCAAGTGGAGACTTTTCCCTCAACTCATTTTGA
 CTATCCCTGTGAAAAGAATAGCTGTTAGTTTCTGAAATGGGCTTTTCTGAAATGGGCTA
 TCGCTACCATGTGTTGTTGTCATCACAGGTGTTGCCCTGCAACGTAAACCAAGTGGTGG
 TCCCTGCCACAGAAGAATAAAAGTACCTTATTCTCAAAAAAAAAAAAAAA

FIGURE 248

MVFLPLKWSLATMSFLLSSLLALLTVSTPSWCQSTEASPKRSDGTPFPWNKIRLPEYVIPVH
YDLIHLANLTTLFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPLQVLE
HPPQEQLALLAPEPLLVLGPLYTVVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTA
ARMAFPCFDEPAFKASFISIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMSTYLVA
FIISDFESVSKITSGVKVSVYAVPDKINQADYALDAAVTLLFYEDYFSIPYPLPKQDLAA
IPDFQSGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVAHELHQWFGNLVTMEWWNDL
WLNEGFAKFMEFVSVSVTHPELKVGDYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFD
DVSYDKGACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICPTDGVKGMDG
FCRSRSQHSSSSSHWHQEGDVKTMMNTWTLQRGFPLITITVRGRNVHMKQEHYMKGSDGAPD
TGYLWHVPLTFITSKSNMVHRFLLKTKTDVLILPEEVEWIKFNVGMNGYYIVHYEDDGWDSL
TGLLKGHTAVSSNDRASLINNAFQLVSIGKLSIEKALDLSELYLKHETEIMPFQGLNELIP
MYKLMEKRDNEVETQFKAFIRLLRDLIDKQTWTDEGSVSEQMLRSELLLLACVHNYQPCV
QRAEGYFRKWKESNGNLSLPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSSTEKSQIEFALC
RTQNKEKLQWLDESFKGDKIKTQEFPQILTIGRNPVGYPLAWQFLRKNWNKLVQKFELGS
SSIAHMVMGTTNQFSTRTRLEEVKGFFSSLKENGSQLRCVQQTIETIEENIGWMDKNFDKIR
VWLQSEKLERM

Signal peptide:

amino acids 1-34

N-glycosylation sites:

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

Neutral zinc metallopeptidases, zinc-binding region signature:

amino acids 350-360

FIGURE 249

CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCCAC
 TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTGGACAGTTCAGCATGTGTGGAAGGTGTCC
 GACCTACCCCGCAATGGACCCCTAAGAACACACCAGCTGCGACAGCGGCTTGGGTGCCAGGA
 CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGTCTCCAAGGGCTGCACGG
 AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCGCCTCTCCCTGATC
 TCCTACACCTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCGCT
 TTGGGCCAACAGCCCCCAGCAGACCCAGGATCCTGAGGTGCCAGTCTGCTTGTCTATGG
 AAGGCTGTCTGGAGGGACAACAGAACAGAAGAGATCTGCCCAAGGGGACCACACACTGTTATGAT
 GCCCTCCTCAGGCTCAGGGGAGGAGGCATCTCTCCAATCTGAGAGTCCAGGGATGCATGCC
 CCAGCCAGGTTGCAACCTGCTCAATGGACACAGGAAATTGGGCCGTGGTATGACTGAGA
 ACTGCAATAGGAAAGATTCTGACCTGTCACTGGGGACCACCATTATGACACACGGAAAC
 TTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGCAGGT
 GTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGACAAAAG
 GCTGCAGCACTGTTGGGCTCAAAATTCCCAGAACGACCACCATCCACTCAGCCCCCTGGG
 GTGCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG
 CAGCGTTCTGCTGAACCTCCCTCCCTCAAGCTGCCCTGTCCCAGGAGACGGCAGTGTG
 CTACCTGTGTGCAGCCCCCTGGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCAGG
 GGCGCCACTCATTGTTATGATGGGTACATTCTCTCAGGAGGTGGCTGTCCACCAAAAT
 GAGCATTCAAGGCTCGGTGGCCAACCTCCAGCTTCTGTTGAACCACACCAGACAAATCG
 GGATCTTCTCTGCGCGTGAGAACGCGTATGTGCAAGCCTCCTGCCTCTCAGCATGAGGGAGGT
 GGGGCTGAGGGCTGGAGTCTCTCACTTGGGGGTGGGCTGGCACTGGCCCCAGCGCTGTG
 GTGGGGAGTGGTTGCCCTCCTGCTTAACTCTATTACCCCCACGATTCTCACCGCTGCTGA
 CCACCCACACTCAACCTCCCTGACCTCATAACCTAATGGCCTGGACACCAGATTCTTC
 CCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCTATCTACTCACCTAACAGCA
 AACACTGGGGAGAGCCTGGAGCATCCGGACTTGCCTATGGGAGAGGGACGCTGGAGGAGTG
 GCTGCATGTATCTGATAATACAGACCCCTGTCTTCA

FIGURE 250

MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLMLI
ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCMPPGCGN
LLNGTQEIGPGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTSNTEMCEVGQVCQETL
LIIDVGLTSTLVGTVKGCVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSVLLN
SLPPQAAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGVGLALAPALWWGVVC
PSC

FIGURE 251

GCGACGGGCAGGACGCCCGTTCGCCTAGCGCGTGTCAAGGAGTTGGTGTCCCTGCCTGCGCT
 CAGGATGAGGGGAATCTGGCCCTGGTGGCGTTCTAATCAGCCTGGCCTTCCTGTCACTGCTG
 CCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCCTGCTCTGTGCAGATCCTCGTCCCTGG
 CCTCAAAGGGATGCAGGGAGAGAAAGGGAGACAAAGGCCCGGACGCCCTGGAAGAGTCG
 GCCCCACGGGAGAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGTGTGGTCGTCA
 GGAAAAATTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGGTGACATAGGACCCCC
 TGGTCCTAATGGAGAACCAAGGCCTCCCATGTGAGTGCAGCCAGCTGCGCAAGGCCATGGGG
 AGATGGACAACCAGGTCTCAGCTGACCAGCGAGCTCAAGTTCATCAAGAATGCTGTCGCC
 GGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAGGAGGAGAACGCGTACGCGGA
 CGCCCCAGCTGTCCGCCAGGGCCGGGGCACGCTGAGCATGCCAAGGACGAGGCTGCCA
 ATGGCCTGATGGCCGCATAACCTGGCGCAAGCCGCCTGGCCGTCTTCATCGGCATCAAC
 GACCTGGAGAAGGAGGGCCCTCGTGTACTCTGACCACTCCCCATGCGGACCTCAACAA
 GTGGCGCAGCGGTGAGCCAACAATGCCTACGACGAGGAGACTGCGTGGAGATGGTGGCCT
 CGGGCGGCTGGAACGACGTGGCCTGCCACACCACCATGTACTTCATGTGAGTTGACAAG
 GAGAACATTGAGCCTCAGGCTGGGCTGCCATTGGGGCCCCACATGTCCTGCAGGGTT
 GGCAGGGACAGAGCCAGACCATGGTGCCAGCCAGGGAGCTGTCCTCTGTGAAGGGTGGAG
 GCTCACTGAGTAGAGGGCTGTTGTCTAAACTGAGAAAATGGCCTATGCTTAAGAGGAAAATG
 AAAGTGTCCCTGGGTGCTGTCTCTGAAGAACGAGAGTTCATTACCTGTATTGTAGCCCCA
 ATGTCATTATGTAATTATTACCCAGAATTGCTCTTCCATAAAGCTTGTGCCTTGTC
 TATACAATAAAATCTTAAGTAGTGCAGTAGTTAAGTCCAAAAAAAAAAAAAAA

0 9 8 7 6 5 4 3 2 1 0

FIGURE 252

MRGNLALVGVLISLAFLSLLPSGHQPAGDDACSVQILVPGKGDAGEKGDKGAPGRPGRVG
PTGEKGDMGDKQKGSGVGRHGKIGPIGSKGEKGDSGDIGPPGPNGEPGLPCECSQLRKAIGE
MDNQVSQLTSELKFIFKNAVAGVRETESKIYLLVKEEKRYADAQLSCQGRGGTLSMPKDEAAN
GLMAAYLAQAGLARVFFIGINDLEKEGAFVYSDHSPMRTFNKWRSGEPNNAYDEEDCVELVAS
GGWNDVACHTTMYFMCEFDFKENM

FIGURE 253

AGTGAUTGCAGCCTTCAGATCCCCTCCACTCGGTTCTCTCTTTGCAGGAGCACCGGCAG
CACCAAGTGTGTGAGGGGAGCAGGCAGCGGTCTAGCCAGTTCTTGATCCTGCCAGACCACC
CAGCCCCGGCACAGAGCTGCTCCACAGGCACC**ATG**AGGGATCATGCTGCTATTACAGCCAT
CCTGGCCTTCAGCCTAGCTCAGAGCTTGGGCTGTCTGTAAGGAGCCACAGGAGGGTGG
TTCCTGGCGGGGGCCGCAGCAAGAGGGATCCAGATCTCTACCAAGCTGCTCCAGAGACTCTTC
AAAAGCCACTCATCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAA
GGAATCAACATCTCCGAGAACGTGACATGCATGACTTCTTGAGGACTTATGGCAAGA
GGAGCGTCCAGCCAGAGGGAAAGACAGGACCTTCTACCTTCAGTGAGGGTTCTCGGCC
CTTCATCCAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGAACAGAGGAGCAGAGACC
TTTA**TAA**GACTCTCCTACGGATGTGAATCAAGAGAACGTCCCCAGCTTGGCATCCTCAAGT
ATCCCCCGAGAGCAGAATAGGTACTCCACTTCCGGACTCCTGGACTGCATTAGGAAGACCTC
TTTCCCTGTCCCATTCCCCAGGTGCGCACGCTCCTGTTACCTGACCCTGGTGTGAAACTGCA
AACATTCTTGTGCTTGACTCCTCTCCATCTTCTACCTGACCCTGGTGTGAAACTGCA
TAGTGAATATCCCCAACCCCAATGGCATTGACTGTAGAATACCCTAGAGTTCCTGTAGTGT
CCTACATTAAAAATATAATGTCTCTCTATTCCCAACAATAAAGGATTTGCATATGAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 254

MRIMLLFTAILAFSLAQSGAVCKEPQEEVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLK
ALSQASTDPKESTSPEKRDMDFFVGLMGKRSVQPEGKTGPFLPSVRVPRPLHPNQLGSTGK
SSLGTEEQRPL

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

Amidation site.

amino acids 90-94

Leucine zipper pattern.

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

FIGURE 255

GGGCGTCTCCGGCTGCTCCTATTGAGCTGTCTGCTCGCTGTGCCCGCTGTGCCTGCTGTGCC
 CGCGCTGTCGCCGCTGCTACCGCGTCTGCTGGACGCCAGCGAGCTGGTATTG
 GAGCCCTGCGGAGAGCTCAAGGCCAGCTCTGCCAGGAGCCCAGGCTGCCCGTGAGTC
 CCATAGTTGCTGCAGGAGTGGAGCC**ATG**AGCTGCGTCTGGTGGTGTATCCCCTTGGGC
 TGCTGTTCTGGTCTGCCGATCCAAAGGCTACCTCTGCCAACGTCACTCTTAGAGGGAG
 CTGCTCAGCAAATACCAGCACAAACGAGTCTCACTCCGGTCCGAGAGCCATCCCCAGGGA
 GGACAAGGAGGAGATCCTCATGCTGCACAACAAGCTTCGGGCCAGGTGCAGCCTCAGGCCT
 CCAACATGGAGTACATGGTGAGCGCCGGCTCCGGCCGCAGAGGCTGGCACCGGGGTGGGC
 CTGGGCCACCAGCCTGCTCTGTTCCCCAGCCAGCTCTGTTCCCCAGCCAGTGCCTGTGATGG
 CTGGCTCAGGGTCTCCTCTGGCAGGGGAGGATCCGGCTCTGTTCTGTTGTTGTTGTT
 TTGAGACAGGGTCTCACTCTGCCACTGACGCTGGAGTGCAATGGCACAAATCGTCATGCCCTG
 AACAC**TAG**ACTCCGGGTTAAGCGATCCTGCTCAGCCTCCAAGTAGCTGGAACCTACAG
 GCATGCACCATGGTCCCAGCTAGATTTAAATATTTGTGGAGATGGGGTCTGCTACGT
 TGCCCAGGCTGGTCTTGAACCTCTAGGCTCAAGCAATCCTCTGCCCTCAGCCTCTCAAAGTG
 CTAGGATTATAGGCATGAGTCACCCGTCTGGCTCTGGCTCTGTTCTAACATTCTGCCAAA
 ACAACACACGTGGGTTCCCTGTGCAGAGCCTGCCCTGCTCATGTCACTCTGGTAGC
 TCCACTGGAACACAGCTCTCAGCCTTCCCACCTGGAGGCAGAGTGGGAGGGGCCAGGG
 CTGGGCTTGCTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGCACCACCCGTACTTCTC
 CTTAGCCCGTGTGAGCCTCACTTCCACTGGAGAGTCCTCTCGCTGGTTGCCATGACT
 GTGAGATAAGTCGAGGCTGTGAAGGGCCGGCACAGACTGACCTGCCTCCCCAACCCCTAGG
 CTTGCTAACCGGAAAGGAGCTAACGGTGACAGAACAGCCAAGGTCAACCCTCCGGGT
 GATTGTGATGGGTGTTCCAGGTGTGGTGGCGATGCTGCTACTTGACCCCAAGCTCCAGTG
 TGGAAACTCCTCCTGGCTGGTTCCAGAAGTACAGAGGAATGGACCACAGTCTTCCAGG
 GTCCCTCCTCGTCCACCAACGGGAGCCTCCACCTGGCCATCCGTAGCTATGAATGGCTT
 TTTAAACAAACCCACGTCCCAGCCTGGTAACATGGTAAAGCCCCGTCTCACAAAAAAATC
 CAAGTTAGCCGGGATGGTGGTGCACCTGTAGTCCAGCTGCAGTGGACTGAGGTGGAG
 GTGGAGGTGGGGGTGGGAGCTGAGGAAGGAGGATGCTTGAGCCTGGGAAGTCGAGGCTGC
 AGTGAGCTGAGATTGCACCACTGCACTCCAGCCTGGGTGACAGAGCAAGACCCTGTCTAAAAA

FIGURE 256

MSCVLGGVIPLGLLLFLVCGSQGYLLPNVTLLEELLSKYQHNESHSRVRAIPREDKEEILML
HNKLRGQVQPQASNMEYMVSAAGSGRRGWHRGWLGHQPALFSQLCSPASACDGWLRVSSGR
GGSRLCSVLFVCFETGSHSATDAGVQWHNRHALKP

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 27-31, 41-45

N-myristoylation site.

amino acids 126-132, 140-146

Amidation site.

amino acids 85-89

FIGURE 257

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACT**ATGGG**
GTCTGGGCTGCCCTTGTCTCCTCTTGACCCCTGGCAGCTCACATGGAACAGGGCCGG
GTATGACTTTGCAACTGAAGCTGAAGGAGTCTTGACAAATTCTCCTATGAGTCCAGC
TTCCTGGAATTGCTTGAAAAGCTCTGCCTCCTCCATCTCCCTTCAGGGACCAGCGTCAC
CCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA**TGA**CAGCCATTGAAGCCTG
TGTCTTCTTGGCCCGGGCTTTGGCCGGGATGCAGGAGGCAGGCCCGACCCGTCTT
CAGCAGGCCCCACCCCTCCTGAGTGGCAATAAAATTGGTATGCTG

FIGURE 258

MGSGLPLVLLTLLGSSHGTGPGMTLQLKLKESFLTNSSYESSFLELLEKLCLLLHLPSGTS
VTLHHARSQHHVVCNT

FIGURE 259

AATTGTATCTGTGTAATGTTAAAACAAACGAAATAAATAGAAGGAAAAACTTCTGAGTT
CAAAAACAACAGACTAGTACTCTAAAGAACTCTTAAAACAATTAACGTGTTAGGATTGCAGT
TATGATTGGATATTATTAATTCTGTTCTGATGTGGGTTCCACTGTGTTCTGTGTGC
TATTAATATTCACCATTGCAGAACGCTTCATTCACTGTTGAAATGAATGCTTAGTGGATCTG
TGCCTCTACGCATATGTTACAAATTATCTGGAGTCCTAATCAATGCAGAGTCCCCTCCC
CTCCGATTGTTCTAAA**TAATT**GAAAGATGTCGCTGTGGAAAAAGGCATGTATTAAATCTG
TATGATTCTCAACCATTAGTTGGAAAGGTCTTGAAAGCCAATGGAAATACTTTTT
TTTCTTGGCACTAATCAAGTGAGTGTACCTTTCACTTAGTAGGATGTGTTACGCTA
GTAAAATAGAAACCTGTGTTATTCTCAGGTATTTAGAAACAACAGCCATCATTATTT
ATGTGTGTTCTGGCTGTATTCAAAATTATATTTGGGCTATCAAATATTACTTCAT
TCAATATAAAATAACAATAGTAGAAGTTGTTACTTAGATATGCTTCTAGTTGCATTTCTC
AGCCTATGTAAGACTACTTGTGTAATAGCCTTGAAATTACAGTACTGTCTCTACTA
TCTTCAGATTACTTGATTCAAATAACCAATTATGTTGTAATTGATATTAATAAAACCAGA
ATAAAAGTTCATATCTACCC

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FIGURE 260

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFVNECLVDLCLLRICYKLSGVPNQCRVPLP
SDCSK

Important features:

Signal peptide:

amino acids 1-29

FIGURE 261

GAGGATTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACCGGAGCCCTTGAGACATCCTT
 GAGAAGAGCCACAGCATAAGAGACTGCCCTGCTGGTGTTCAGGAT**ATG**ATGGTGGCCCTT
 CGAGGAGCTCTGCATTGCTGGTTCTGTCAGCTTCTGCCCGCCGAGTGTAC
 CCAGGACCCAGCCATGGTCATTACATCTACAGCGCTTCGAGTCTGGAGCAAGGGCTGG
 AAAAATGTACCAAGCAACGAGGGCATACATTCAAGAATTCCAAGAGTTCTCAAAAAATATA
 TCTGTATGCTGGGAAGATGTCAGACCTACACAAGTGAGTACAAGAGTGAGTGGGTAACCT
 GGCAGTGAGAGTTGAACGTGCCAACGGGAGATTGACTACATACAATACCTCGAGAGGCTG
 ACGAGTGATCGATCAGAGGACAAGACACTGGCAGAAATGTTGCTCCAAGAAGCTGAAGAA
 GAGAAAAAGATCCGGACTCTGCTGAATGCAAGCTGTGACAACATGCTGATGGGATCAAAGTC
 TTTGAAAATAGTGAAGAAGATGATGGACACACATGGCTCTGGATGAAAGATGCTGTCTATA
 ACTCTCAAAGGGTGTACTTATTAAATTGGATCCAGAAACACACTGTTGGGAATTGCAAAC
 ATACGGGCATTATGGAGGATAACACCAAGCCAGCTCCCCGGAAGCAAATCCTAACACTTC
 CTGGCAGGGAACAGGCCAAGTGATCTACAAAGTTCTATTTCATAACCAAGCAACCT
 CTAATGAGATAATCAAATATAACCTGCAGAAGAGGACTGTGGAAGATCGAATGCTGCTCCA
 GGAGGGGTAGGCCGAGCATTGGTTTACCAAGCAGTCCCCCTCAACTACATTGACCTGGCTGT
 GGATGAGCATGGGCTCTGGGCCATCCACTCTGGGCCAGGCACCCATAGCCATTGGTTCTCA
 CAAAGATTGAGCCGGCACACTGGGAGTGGAGCATTGATGGGATACCCATGCAGAACCCAG
 GATGCTGAAGCCTCATTCCCTTGTGTTGGGTTCTCTATGTGGTCTACAGTACTGGGGCCA
 GGGCCCTCATCGCATCACCTGCATCTATGATCCACTGGGACTATCAGTGAGGAGGACTTGC
 CCAACTTGTCTTCCCCAAGAGACCAAGAACAGTCACTCCATGATCCATTACAACCCAGAGAT
 AAGCAGCTCTATGCCCTGGAATGAAGGAACAGATCATTACAAACTCCAGACAAAGAGAAA
 GCTGCCTCTGAAG**AA**TGCAATTACAGCTGTGAGAAAGAGCACTGTGGCTTGGCAGCTGTC
 TACAGGACAGTGAGGCTATAGCCCCCTCACAAATATAGTATCCCTCTAATCACACAGGAAG
 AGTGTGTAGAAGTGGAAATACGTATGCCCTTCCCAAATGTCAGTGCCTTAGGTATCTC
 CAAGAGCTTAGATGAGAGCATATCATCAGGAAAGTTCAACAATGTCCATTACTCCCCAAA
 CCTCCTGGCTCTCAAGGATGACCACATTCTGATACAGCCTACTTCAAGCCTTTGTTTACT
 GCTCCCAGCATTACTGTAACTCTGCCATCTCCCTCCCAAATTAGAGTTGTATGCCAGC
 CCCTAATATTCAACCAGTGGCTTCTCTCCCTGGCCTTGCTGAAGCTTCTCCCTTT
 CAAATGTCTATTGATATTCTCCATTTCAGTGCCTTCAACTAAACTATTAAATATTCTT
 CTTTCTTTCTTTTGAGACAAGGTCTCACTATGTTGCCCAGGCTGGTCTCAAACACTCC
 AGAGCTCAAGAGATCCTCCTGCCTCAGCCTCTAAGTACCTGGGATTACAGGCATGTGCCAC
 CACACCTGGCTAAATACTATTCTTATTGAGGTTAACCTCTATTCCCTAGCCCTGTC
 CTTCCACTAAGCTGGTAGATGTAATAATAAAAGTGAAAATATTAAACATTGAAATATCGCTT
 CCAGGTGTGGAGTGTGACATCATTGAATTCTCGTTCACCTTGAGTAAACACAATTACAAAGTGAAGAGATACAGC
 TCTTACAGCTGTCATTCTAGAGTTAGGTGAGTAACACAATTACAAAGTGAAGAGATACAGC
 TAGAAAATACTACAAATCCCAGTCTTCAATTGCCAAGGAAGCATCAAATACGTATGTT
 TGTTCACCTACTCTTATAGTCATGCGTTCATCGTTCAGCCTAAAGATAATAGTCTGTCCC
 TTAGCCAGTTTCAATGTCGACAAGACCTTCAATAGGCCTTCAATGATAATTCCCTCC
 AGAAAACCAAGTCTAAGGGTGAGGACCCCAACTCTAGCCTCTTGTCTGTCTGT
 TTCTCTTTCTGCTTAAATTCAATAAAAGTGACACTGAGCAAAAAAAAAAAAAA

FIGURE 262

MMVALRGASALLVLFLAAFLLPPPQCTQDPAMVHYIYQRFRVLEQGLEKCTQATRAYIQEFQE
FSKNISVMLGRCQTYTSEYKSAVGNLALRVERAQRREIDYIQLREADECIVSEDKTLAEMLL
QEAEKKIRTLNASCDNMLMGIKSLKIVKKMMDTHGSWMKDAVYNSPKVYLLIGSRNNTV
WEFANIRAFMEDNTKPAPRKQILTLSWQGTGQVIYKGFLFFHNQATSNEIIKYNLQKRTVED
RMLLPGGVGRALVYQHSPSTYIDLAVDEHGLWAIHSGPGTHSHLVLTIEPGTLGVEHSWDT
PCRSQDAEASFLLCGVLYVVYSTGGQGPHRITCIYDPLGTISEEDLPNLFFPKRPRSHSMIH
YNPRDKQLYAWNEGNQIIYKLQTKRKLPLK

FIGURE 263

GGGCGCCCGTACTCACTAGCTGAGGTGGCAGTGGTCCACCAAC**ATG**GAGCTCTCGCAGA
 TGTGGAGCTCATGGGGCTGCGGTGTTGCTGGCTGCTGGCCCTGATGGCGACGGCGGCG
 GTAGCGGGGGTGGCTGCGCGGGGGAGGAGAGGAGCGGCCGGCCCTGCCAAAAAGC
 AAATGGATTTCACCTGACAAATCTCGGATCCAAGAACAGAAACATATCAGCGGATT
 GGAAGGAGAACGCTCAACAACACAACCTCACCCACCGCCTCCTGGCTGCAGCTCTGAAGAGC
 CACAGCAGGGAACATATCTTGATGGACTTAGCAGCAATGGCAAATACCTGGTACCTGTGC
 AGATGATCGCACCATCCGCATCTGGAGCACCAGGACTTCCTGCAGCGAGAGCACCGCAGCA
 TGAGAGCCAACGTGGAGCTGGACACGCCACCCCTGGTGCCTCAGCCCTGACTGCAGAGCC
 TTCATCGTCTGGCTGGCCAACGGGGACACCCCTCGTGTCTCAAGATGACCAAGCAGGGAGGA
 TGGGGGCTACACCTCACAGCCACCCAGAGGACTTCCCTAAAAGCACAAGGCCCTGTCA
 TCGACATGGCATGCTAACACAGGAAGTTATCATGACTGCCTCAGTGACACCAACTGTC
 CTCATCTGGAGCCTGAAGGGTCAAGTGTCTACCATCAACACCAACCAGATGAACAACAC
 ACACGCTGCTGTATCTCCCTGTGGCAGATTGAGCTCGTGTGGCTTCACCCAGATGTGA
 AGGTTTGGGAAGTCTGTTGGAAAGAAGGGGAGTTCCAGGAGGTGGTGCAGCCTCGAA
 CTAAAGGGCACTCCGGCTGTGCACTCGTTGCTTCTCCAACGACTCACGGAGGATGGC
 TTCTGTCTCCAAGGATGGTACATGGAAACTGTGGGACACAGATGTGGAATACAAGAAGAAGC
 AGGACCCCTACTTGCTGAAGACAGGCCCTTGAAGAGGCAGGGTGCCTGCGCCGTGCC
 CTGGCCCTCTCCCCAACGCCAGGTCTGGCCTGGCCAGTGGCAGTAGTATTCTCATCTCA
 CAATACCCGGCGGGCGAGAAGGAGGAGTGCTTGAGCGGGTCCATGGCAGTGATCGCCA
 ACTTGCTCTTGACATCACTGGCCCTTCTGGCCTCCTGTGGGGACCGGGCGGTGCGGCTG
 TTTCACACACTCCTGGCACCAGGCATGGTGGAGGAGATGCAGGGCACCTGAAGCGGGC
 CTCCAACGAGAGCACCCGCCAGGGCTGCAGCAGCAGCTGACCCAGGCCAACAGAGACCC
 AGAGCCTGGGTGCCCTGAAGAAG**TCA**CTCTGGAGGGCCGGCGCAGAGGATTGAGGAGGAG
 GGATCTGGCCTCCTCATGGCACTGCTGCCATCTTCCCTCCAGGTGGAAGCCTTCAGAAGG
 AGTCTCTGGTTTCTTACTGGTGGCCTGCTTCTTCCATTGAAACTACTCTTGCTACTT
 AGGTCTCTCTTCTGCTGGCTGTGACTCCTCCCTGACTAGTGGCCAAGGTGCTTTCTTC
 CTCCCAGGCCAGTGGTGGAATCTGCCCCACCTGGCACTGAGGAGAATGGTAGAGAGGAG
 AGGAGAGAGAGAGAGAATGTGATTTGGCCTGTGGCAGCACATCCTCACACCCAAAGAAG
 TTTGTAAATGTTCCAGAACACCTAGAGAACACCTGAGTACTAAGCAGCAGTTGCAAGG
 TGGGAGACTGGGATAGCTTCCATCACAGAACTGTGTTCCATAAAAAGACACTAAGGGATT
 TCCTTCTGGCCTCAGTTCTATTTGTAAGATGGAGAATAATCCTCTGTGAACCTTGCA
 AAGATGATATGAGGCTAACAGAGAATATCAAGTCCCCAGGTCTGGAAGAAAAGTAGAAAAGAGT
 AGTACTATTGTCCAATGTCATGAAAGTGGTAAAAGTGGGAACCAAGTGTGCTTTGAAACCAA
 TTAGAAACACATTCTGGAGGCAAAGTTCTGGACTTGATCATACATTATATGGT
 TGGGACTCTCTCTGGAGATGATATCTGTTAAGGAGACCTCTTCAGTTCATCAAG
 TTCATCAGATATTGAGTGCCACTCTGTGCCAAATAAATATGAGCTGGGATTAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 264

MELSQMSELMGLSVLLGLLALMATAAVARGWLRAEERSGRPACQKANGFPPDKSSGSKKQK
QYQRIRKEKPQQHNFTHRLLAAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQ
REHRSMRANVELDHATLVRFSPDCRAFIWVLANGDTLRFVKMTKREDGGYTFTATPEDFPKK
HKAPVIDIGIANTGKFIMTASSDTTVLIWSLKGQVLSTINTNQMNNTHAAVSPCGRFVASCG
FTPDPKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKDGTWKLWDTDV
EYKKKQDPYLLKTGRFEAAAGAAPCRLALSPNAQVLALASGSSIHLYNTRRGEKEECFERVH
GECIANLSFDITGRFLASCGDRAVRLFHNTPGHARAMVEEMQGHLKRASNESTRQLQQQLTQ
AQETLKSLGALKK

Important features:

Signal peptide:

amino acids 1-25

N-glycosylation site.

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

Beta-transducin family Trp-Asp repeat protein.

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

FIGURE 265

TGGCCTCCCCAGCTTGCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAACGAGG
CAGTGTTTGCCTCACCCCAAGTGACC**ATGAGAGGTGCCACCGAGTCTCAATCATGCTCC**
TCCTAGTAACTGTGTCTGACTGTGCTGTGATCACAGGGGCCTGTGAGCGGGATGTCCAGTGT
GGGCAGGCACCTGCTGTGCCATCAGCCTGTGGCTCGAGGGCTGCGGATGTGCACCCCGCT
GGGGCGGGAAAGGCGAGGGAGTGCCACCCCGCAGCCACAAGGTCCCCTTCTCAGGAAACGCA
AGCACCACACCTGTCCTGCTTGCCTAACCTGCTGTGCTCCAGGTTCCGGACGGCAGGTAC
CGCTGCTCCATGGACTTGAAGAACATCAATT**TAG**CGCTTGCCTGGTCTCAGGATAACCA
CCATCCTTTCTGAGCACAGCCTGGATTTTATTCGCCATGAAACCCAGCTCCATGAC
TCTCCCAGTCCCTACACTGACTACCCCTGATCTCTCTGTCTAGTACGCACATATGCACACAG
GCAGACATACCTCCCATCATGACATGGTCCCCAGGCTGGCTGAGGATGTCACAGCTTGAGG
CTGTGGTGTGAAAGGTGCCAGCCTGGTTCTTCCCTGCTCAGGCTGCCAGAGAGGTGGTA
AATGGCAGAAAGGACATTCCCCCTCCCTCCCCAGGGTGCACCTGCTCTTCCCTGGGCCCTG
CCCCTCTCCCCACATGTATCCCTCGGTCTGAATTAGACATTCCCTGGCACAGGCTTTGGGT
GCATTGCTCAGAGTCCCAGGTCTGGCCTGACCCCTCAGGCCCTCACGTGAGGTCTGTGAGG
ACCAATTGTGGTAGTTCATCTTCCCTCGATTGGTTAACCTCTAGTTTAGACACCACAGAC
TCAAGATTGGCTCTTCCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCA
GGGAGGCAATCAGCCCCCTGAAGACTCTGGTCCCAGTCAGCCTGTGGCTGTGGCCTGTGA
CCTGTGACCTTCTGCCAGAATTGTCATGCCTCTGAGGCCCTCTTACACACTTACAGT
TAACCACGTGAAGCCCCAATTCCCACAGCTTCCATTAAAATGCAAATGGTGGTGGTCAA
TCTAATCTGATATTGACATATTAGAAGGCAATTAGGGTGTTCCTAAACAACCTCTTCCA
AGGATCAGCCCTGAGAGCAGGTGGTACTTGAGGAGGGCAGTCCTCTGTCCAGATTGGGG
TGGGAGCAAGGGACAGGGAGCAGGGCAGGGCTGAAAGGGCAGTCATTGAGCACCAACTGGGAGG
CAACTACACACCAACATGCTGGCTTGAATAAAAGCACCAACTGAAAAAA

FIGURE 266

MRGATRVSIMLLVTVDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHP
GSHKVPFFRKHKHTCPCLPNLLCSRFPDGRYRCSDLKNINF

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site:

amino acids 88-95

N-myristoylation sites:

amino acids 33-39, 35-41, 46-52

FIGURE 267

AGCGCCGGCGTCGGGCGGTAAAAGGCCGCAGAAGGGAGGCACTTGAGAA**ATG**TCTTC
 CTCCAGGACCAAGTTCTCACCATGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGC
 TGCTGCCTTGGCATTGCTGCTGCCAACACAGACGTGTTCTGTCCAAGCCCCAGAAAGCGG
 CCCTGGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAAGGAACCAAGGACTTCAA
 GCAAAGGAGCTATGGAAAAAAATGGAGCTGTGATTATGCCGTGCGGAGGCCAGGCTGTT
 CCTCTGTCGAGAGGAAGCTGCGGATCTGTCCTCCCTGAAAAGCATGTTGGACCAGCTGGCG
 TCCCCCTCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTCCAGCCTTAT
 TTCAAAGGAGAAATCTCCTGGATGAAAAGAAAAGTTCTATGGTCCACAAAGGCGGAAGAT
 GATGTTATGGGATTATCCGTCTGGAGTGTGGTACAACCTCTCCGAGCCTGGAACGGAG
 GCTTCTCTGAAACCTGGAAGGAGAAGGCTTCATCCTGGGGAGTTTGTGGTGGGATCA
 GGAAAGCAGGGCATTCTCTTGAGCACCGAGAAAAAGAATTGGAGACAAAGTAAACCTACT
 TTCTGTTCTGGAAGCTGCTAAGATGATCAAACACAGACTTGGCCTCAGAGAAAAAA**TGA**T
 TGTGTGAAACTGCCAGCTCAGGGATAACCAGGGACATTCACCTGTGTTATGGGATGTATT
 GTTCCACTCGTGTCCCTAAGGAGTGAGAAACCCATTATACTCTACTCAGTATGGATTA
 TTAATGTATTTAATATTCTGTTAGGCCACTAAGGCAAATAGCCCCAAACAAGACTGA
 CAAAAATCTGAAAAACTAATGAGGATTATTAAGCTAAACCTGGAAATAGGAGGCTTAAA
 TTGACTGCCAGGCTGGGTGCAGTGGCTCACACCTGTAATCCCAGCACTTGGGAGGCCAAGG
 TGAGCAAGTCACTTGAGGTGGAGTTGAGACCCAGCCTGAGCAACATGGCGAAACCCCGTC
 TCTACTAAAATACAAAATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCAGCTACCCG
 GGAGGCTGAGGCAGGAGAATCACTGAACCTGGGAGGTGGAGGTTGCGGTGAGCTGAGATCA
 CACCACTGTATTCCAGCCTGGGTGACTGAGACTCTAACTAA

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FIGURE 268

MSFLQDPSFFTGMWSIGAGALGAAALALLANTDVFLSKPQKAALEYLEDIDLKTLEKEPR
TFKAKELWEKNGAVIMAVRRPGCFLCREEAIDLSSLKSMLDQLGVPLYAVVKEHIRTEVKDF
QPYFKGEIFLDEKKKFYGPQRKMMFMGFIRLGWYNFFRAWNGGFSGNLEGEgefILGGVFV
VGSGKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

FIGURE 269

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCG
GGCCAGGTGCCCGTCGCAGGTGCCCTGGCCGGAGATGCGGTAGGAGGGCGAGCGCGAGA
AGCCCCTCCTCGGCCTGCCAACCGCCACCCAGCCC**ATG**GCGAACCCGGCTGGGCTG
CTTCTGGCGCTGGGCTGCCGTTCTGCTGCCCGCTGGGCCGAGCCTGGGGCAAATACA
GACCACTTCTGCAAATGAGAATAGCACTGTTGCCTCATCCACCACTCCAGCTCCGATG
GCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTCTCCCTTGGCTGCCTTG
CTCCTGGCTGTGGGCTGGCACTGTTGGTGCAGCTTCGGAGAAGCGGCAGACGGAGGG
CACCTACCGGCCAGTAGCGAGGAGCAGTTCTCCATGCAGCCGAGGCCGGCCCTCAGG
ACTCCAAGGAGACGGTGCAGGGCTGCCATC**TAG**GTCCCCCTCCTGCATCTGTCTCC
CTTCATTGCTGTGACCTGGGAAAGGCAGTGCCTCTGGCAGTCAGATCCACCCAG
TGCTTAATAGCAGGGAAAGAAGGTACTCAAAGACTCTGCCCTGAGGTCAAGAGAGGATGGG
GCTATTCACTTTATATATTATAAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAA

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FIGURE 270

MANPGLGLLLALGLPFLLARWGQIQTTSANENSTVLPSSSTSSSDGNLRPEAITAII
VFSLLAALLLAVGLALLVRKLREKRQTEGYRPSSEEQFSAEEARAPQDSKETVQGCLPI

FIGURE 271

AATATATCATCTATTATCATTAAATAATGTATTCTTTATTCCAATAACATTTGGGTT
TTGGGATTTAATTTCAAACACAGCAGA**ATG**ACATTCTGTCACTATTATTATTGTTG
GTATGTGAAGCTATTGGAGATCCAATTCAAGGAAGCAACACATTGGAGAATGGCTACTTCT
ATCAAGAAATAAAGAGAACCAACAGTCACCCACACAATCATCTTAGAAGACAGTGTGACTC
CTACCAAAGCTGTCAAAACCACAGGCAAGGCATAGTTAAAGGACGGAATCTGACTCAAGA
GGGTTAATTCTTGGTGCTGAAGCCTGGGCAGGGGTGTAAGAAAAACACT**TAG**ATTCAATG
ATTGTAAATTAAAGGCAAATACACATATTAGTATTACCTTAGTGTAAATGTATCCCTGTCATA
TATACAATAAGGTGAAATTATAAGTACCCATGCAGTTGGCTGGACAGTTCTAAATTGGACT
TTATTAATTTAAAATCAGTAACTGATTATCACTGGCTATGTGCTTAGATCTACAGGAGA
TCATATAATTGATAACAATAAAAGAAAAGTGTCTCTCCCCTACAGAATTGACATTAA
ATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAA
AGAAGGAAAATGTTGCCAAGGAAAAAA

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FIGURE 272

MTFFLSLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGK
GIVKGRNLDSRGLILGAEAWGRGVKKNT

FIGURE 273

GCCAGGAATAACTAGAGAGGAACA**ATG**GGGTATTCAAGAGGTTTGTTCCTCTAGTTCT
 GTGCCTGCTGCACCAGTCAAACTCTCCTCATTAAGCTGAATAATAATGGCTTGAAGATA
 TTGTCAATTGTTAGATCCTAGTGTGCCAGAAGATGAAAAAATAATTGAACAAATAGAGGAT
 ATGGTGAACAGCTCTACGTACCTGTTGAAGCCACAGAAAAAGATTTTTCAAAA
 TGTATCTATATTAACTCCTGAGAATTGGAAGGAAATCCTCAGTACAAAAGGCCAAACATG
 AAAACCATAAACATGCTGATGTTAGTTGCCACACCTACACTCCCAGGTAGAGATGAACCA
 TACACCAAGCAGTCACAGAATGTGGAGAGAAAGGCGAATACATTCACTCACCCCTGACCT
 TCTACTTGGAAAAAAACAAAATGAATATGGACCACCCAGGCAAACACTGTTGTCCATGAGTGG
 CTCACCTCCGGTGGGAGTGTGAGTACAATGAAGATCAGCCTTCTACCGTGCTAAG
 TCAAAAAAAATCGAACAAAGGTGTTCCGCAGGTATCTCTGGTAGAAATAGAGTTATAA
 GTGTCAAGGAGGGCAGCTGCTTAGTAGAGCATGCAGAATTGATTCTACAAACAAACTGTATG
 GAAAAGATTGTCAATTCTTCCTGATAAAGTACAAACAGAAAAGCATCCATAATGTTATG
 CAAAGTATTGATTCTGTTGAATTGTAACGAAAAAACCCATAATCAAGAAGCTCCAAG
 CCTACAAAACATAAGTCAATTAGTACATGGGAGGTGATTAGCAATTCTGAGGATT
 TTAAAAAACACCATAACCATGGTGACACCACCTCCTCACCTGTCTCTCATTGCTGAAGATC
 AGTCAAAGAATTGTGTGCTTAGTTCTGATAAGTCTGGAGCATGGGGGTAAGGACCGCCT
 AAATCGAATGAATCAAGCAGCAAACATTTCTGCTGAGACTGTTGAAAATGGATCCTGG
 TGGGGATGGTCACTTGATAGTACTGCCACTATTGTAATAAGCTAATCCAAAATAAAAGC
 AGTGTGAAAGAACACACTCATGGCAGGATTACCTACATATCCTCTGGGAGGAACCTCCAT
 CTGCTCTGGAATTAAATATGCATTTCAGGTATTGGAGAGCTACATTCCAACACTGATGGAT
 CCAGTACTGCTGACTGATGGGGAGGATAAACACTGCAAGTTCTGTATTGATGAAGTG
 AAACAAAGTGGGCCATTGTTCAATTGTTATTGCTTTGGAGAGCTGCTGATGAAGCAGTAAT
 AGAGATGAGCAAGATAACAGGGAGAAGTCATTTTATGTTCAGATGAAGCTCAGAACAAATG
 GCCTCATTGATGCTTTGGGCTCTACATCAGGAAACTGATCTCTCCAGAAGTCCCT
 CAGCTGAAAGTAAGGGATTAACACTGAATAGTAATGCCGGATGAACGACACTGTCATAAT
 TGATAGTACAGTGGAAAGGACACGTTCTTCATCACATGGAACAGTCTGCCCTCAGTA
 TTTCTCTGGGATCCCAGTGGAAACAATAATGGAAAATTTCACAGTGGATGCAACTTCCAAA
 ATGGCCTATCTCAGTATTCCAGGAACCTGCAAAGGTGGCACTTGGCATAACATCTCAAGC
 CAAAGCGAACCCAGAAACATTAACATTACAGTAACCTCTGAGCAGCAAATTCTCTGTGC
 CTCCAATCACAGTGAATGCTAAATGAATAAGGACGTAAACAGTTCCAGGCCAATGATT
 GTTTACGAGAAAATTCTACAAGGATATGTAACCTGCTTGGAGCCAATGTGACTGCTTCA
 TGAATCACAGAATGGACATACAGAAAGTTGGAAACTTTGGATAATGGTGCAGGGCGCTGATT
 CTTTCAAGAATGATGGAGTCACTCCAGGTATTTACAGCATATACAGAAAATGGCAGATAT
 AGCTTAAAGTTCGGGCTCATGGAGGAGCAAACACTGCCAGGCTAAATTACGGCCTCCACT
 GAATAGAGCCCGTACATACCAGGTGGTAGTGAACGGGAAATTGAAGCAAACCCGCCAA
 GACCTGAAATTGATGAGGAACTCAGACCACCTGGAGGATTTCAGCCGAACAGCATCCGGA
 GGTGCATTGTTGATCACAAGTCCCAAGCCTTCCCTGCTGACCAATACCCACCAAGTCA
 AATCACAGACCTGATGCCACAGTTCATGAGGATAAGATTATTCTACATGGACAGCACCAG
 GAGATAATTGATGTTGGAAAAGTCAACGTTATATCATAAGAATAAGTGAAGTATTCTT
 GATCTAAGAGACAGTTGATGATGCTCTCAAGTAAATACTACTGATCTGTCACCAAAGGA
 GGCCAACTCCAAGGAAAGCTTGCATTAAACAGAAAATCTCAGAAGAAAATGCAACCC
 ACATATTATTGCCATTAAAGTATGATAAAAGCAATTGACATCAAAGTATCCAACATT
 GCACAAGTAACCTTGTATTCCCTCAAGCAAATCCTGATGACATTGATCTACACCTACTCC
 TACTCCTACTCCTACTCCTGATAAAAGTCATAATTCTGGAGTTAATTATTCTACGCTGGTAT
 TGTCTGTGATTGGGCTGTTGAATTGTTACTTTATTGTTATTGTAAGAAAATAGTGTGAA
 ACACGAAAGAAAAAAATCTCAAGTAGACCTAGAAGAGAGTTTAAAAACAAAATGTAAGT
 AAAGGATATTCTGAATCTAAAATTCCATGTGTGATCATAAAACTCATAAAAATAATT
 TTAAGATGTCGGAAAAGGATACTTGATTAAATAAAACACTCATGGATATGAAAAACTGT
 CAAGATTAATTAAGTTCATTATTGTTATTGTTATTGTAAGAAAATAGTGTGAA
 AAAGATCCTTTCTCATACTGATACCTGGTTGATATTATTGATGCAACAGTTCTGAA
 GATATTCTCAAAATTGATCAAGAAATTAAAATCATCTATGAGTAGTCAAAATACAAGTAA
 GGAGAGCAAATAACAAACATTGGAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 274

MGLFRGFVFLVLCLLHQSNNTSFIKLNNNGFEDIVIVIDPSVPEDEKIIEQIEDMVTTASTY
LFEATEKRFFFKNVSILIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTKQFTEC
GEKGEYIHFTPDLILLGKKQNEYGPPGKLFVHEWAHLRGVFDEYNEDQPFYRAKSKKIEATR
CSAGISGRNRVYKCQGGSCLSACRIDSTTKLYGKDCQFFPDKVQTEKASIMFMQSIDSVVE
FCNEKTHNQEAPSLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPPVSLLKISQRIVCLV
LDKSGSMGGKDRLNRMNQAAKHFLQLTVENGSWGMVFDSTATIVNKLIQIKSSDERNTLM
AGLPTYPLGGTSICSGIKYAFQVIGELHSQLDGSEVLLLTDGEDNTASSCIDEVKQSGAIVH
FIALGRAADEAVIEMSKITGGSHFYVSDEAQNNGLIDAEGALTSGNTDLSQKSLQLESKGLT
LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDPSGTIMENFTVDATSKMAYLSIPG
TAKVGTWAYNLQAKANPETLTITVTSRAANSSVPPI TVNAKMNDVNSFPSPMIVYAEILQG
YVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNNDGVYSRYFTAYTENGRYSLKVRAGH
GANTARLKLRRPPLNRAAYIPGWVVNGEIEANPPRPEIDEDTQTTLEDFSRASGGAFVVSQV
PSLPLPDQYPPSQITDLDATVHEDIILTWTAPGDNFDVGKVQRYIIRISASIILRDSFDD
ALQVNTTDLSPKEANSKESFAFKPENISEENATHIFIAIKSIDKSNLTSKVSNIAQVTLFIP
QANPDDIDPTPTPTPTPDKSHNSGVNISTLVLSVIGSVVIVNFILSTTI

Signal peptide:

amino acids 1-21

Putative transmembrane domains:

amino acids 284-300, 617-633

Leucine zipper pattern.

amino acids 469-491, 476-498

N-glycosylation site.

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

FIGURE 275

CTCCTTAGGTGGAAACCTGGGAGTAGAGTACTGACAGCAAAGACCGGGAAAGACCATACTGCCCG
 GGCAGGGGTGACAACAGGTGTCATCTTTGATCTCGTGTGGCTGCCTCTATTTCAAGGAAAG
 ACGCCAAGGTAATTGACCCAGAGGAGCAATGATGTAGGCCACCTCCTAACCTCCCTCTGAACC
 CCCAGTTATGCCAGGATTACTAGAGAGTGTCAACTCAACAGCAAGCGGCTCTCGGCTTAACCT
 GTGGTTGGAGGAGAGAACCTTGTGGGCTGCCCTCTCTAGCAGTGTCAAGAAGTGACTTGCTGA
 GGGTGGACCAAGAAGAAGGAAAGGCTCCCTCTGCTGTGGCTGCACATCAGGAAGGCTGTGATGGG
 AATGAAGGTGAAAAGTGGAGATTCACTCAGTCATTGCTCTGCCTGCAAGATCATCCTTAAAAA
 GTAGAGAAGCTGCTCTGTGTGGTTAACCTCAAGAGGAGAAGCTGTTAGAAGGAAATGGATG
 CAAGCAGCTCCGGGGCCCCAACGCATGCTCCTGTGGTAGGCCAGGGAAAGCCCTCCGTGGG
 GCCCGGCTTGAGGGATGCCCCGGTTCTGGACGCATGGCTGATTCTGAATGATGATGGTTCGCC
 GGGGGCTGCTTGCGTGGATTTCGGGGGGTGGTTGCTGGCTCCTCTGCTGTGCTATCTCTGT
 CCTGTACATGTTGGCCTGCACCCCCAAAAGGGTGCAGGAGGAGCAGCTGGCAGTGGGCAAGGCA
 CCCACGGGAAGGAGGGTACCAAGGCCGTCCTCAGGAGTGGGAGGAGCAGCACCGCAACTACGTGA
 GCAGCCTGAAGCGCAGATCGCACAGCTCAAGGAGGAGCTGCAGGAGAGGAGTGAGCAGCTCAGGAA
 TGGGCAGTACCAAGCCAGCGATGCTGCTGGCCTGGGTCTGGACAGGGAGCCCCCAGAGAAAACCCAG
 GCCGACCTCCTGGCCTCCTGCACTCGCAGGTGGACAAGGCAGAGGTGAATGCTGGCGTCAAGCTGG
 CCACAGAGTATGCAAGCAGTGCCTTCCGATAGCTTACTCTACAGAAGGTGTACCAGCTGGAGACTGG
 CCTTACCCGCCACCCCAGGGAGAACGCTGTGAGGAAGGACAAGCGGGATGAGTTGGGAAGGCCATT
 GAATCAGCCTTGAGGACCTGAACAACTCTGCAGAGAACAGCCCCAACACCGCTTACACGGCCT
 CTGATTTCATAGAAGGGATCTACCGAACAGAAAGGGACAAAGGGACATTGATGAGCTCACCTCAA
 AGGGGACACAAACACGAATTCAAACGGCTCATCTTATTGACCATCAGCCCCATCATGAAAGTG
 AAAAATGAAAAGCTAACATGGCCAACACGCTTATCAATGTTATCGTGCCTCTAGCAAAAAGGGTGG
 ACAAGTCCGGCAGTTCATGCAGAATTTCAGGGAGATGTGCATTGAGCAGGATGGGAGAGTCCATCT
 CACTGTTTACTTTGGGAAAGAAGAAATAAATGAAGTCAAAGGAATACTTGAAGGAAACTTCCAAA
 GCTGCCAACTTCAGGAACTTACCTTCATCCAGCTGAATGGAGAATTTCCTGGGGAAAGGGACTTG
 ATGTTGGAGCCCGTCTGGAGGGAAAGCAACGTCCTCTCTTGTGATGTTGGACATCTACT
 CACATCTGAATTCTCAATACGTGTAGGCTGAATACACAGCCAGGGAAAGAAGGTATTTATCCAGTT
 CTTTCAGTCAGTACAATCCGGATAATATAACGGCCACATGATGCAGTCCTCCCTGGAACAGC
 AGCTGGTCATAAGAAGGAAACTGGATTGGAGAGCTTGGATTGGGATGACGTGTCAGTATCG
 GTCAAGACTTCATCAATATAGGTGGGTTGATCTGGACATCAAAGGCTGGGGGGAGAGGATGTC
 CTTTATCGCAAGTATCTCCACAGCAACCTCATAGTGGTACGGACGCCGTGCGAGGACTCTCCACC
 TCTGGCATGAGAACGCGTGCATGGAGGCTGACCCCCGAGCAGTACAAGATGTGCATGCAGTCCAA
 GGCCATGAACGAGGCATCCCACGGCCAGCTGGCATGCTGGTTCAGGCACGGAGATAGAGGCTCAC
 CTTCGCAAACAGAAACAGAACAGAACAGTAACTGAAACTTCCAGAGAACAGATTGTGGGAGA
 CACTTTCTCTTCTTGCATTAAGTACTGAAAGTGGCTGCAACAGAGAAAAGACTTCCATAAAGGACG
 ACAAAAGAATTGGACTGATGGGTAGAGATGAGAACGCTCCGATTCTCTCTGGGGCTTTTAC
 AACAGAAATCAAATCTCCGTTGCCTGCAAAGTAAACCCAGTGGCACCCTGTGAAGTGTCTGACA
 AAGGCAGATGCTGTGAGATTATAAGCCTAATGGTGTGGAGGTTGATGGTTACAATACACT
 GAGACCTGTTGTTGTGCTCATTGAAATATTGATGATTTAAGAGCAGTTGTAAGGAAATTCT
 TAGCATGAAAGGCAAGCATATTCTCCTCATATGAATGAGCCTATCAGCAGGGCTCTAGTTCTAGG
 AATGCTAAATATCAGAAGGCAGGGAGAGTGGCTTATTGATGACTAGTGAGTACATTAAGTA
 AAATAAAATGGACCAAGAAAAGAAAAGAACATAAATATCGTGCATATTTCCTCCAAAGATTAACCA
 AAAATAATCTGCTTATCTTTGGTTGCTTTAAGGAAAGATACTTGGAGATGCATTATGAGAACTTCA
 GCACATTGGCCTACATTTCATATTGAGGAAACTTGGAGGAAAGAACACTTCTGCTTACAGGAA
 GTTCAAAGCATCAAATTGATGCCATATCCAAGGACATGCCAAATGCTGATTCTGTCAGGCAGTGAAT
 GTCAGGCATTGAGACATAGGAAGGAATGGTTGACTAATACAGACGTACAGATACTTCTCTGAA
 GAGTATTCTGGAGGAGGAGAACACTGAAACACTGGAGGAAAGAAAAGACACTTCTGCTTACAGGAA
 AAGGAAACTCATTGAGACTGGTGTGATATCGTGTGATCTGCTTAAAGGAAAGAACACATTTCCTCA
 GAAGTAGGGACCGCCTTCTTACCTGTTAAATAAACCCTAAAGTATACCGTGTGAACCAAAACATCT
 TTTCAAACAGGGTGCTCTGCCGCTTCTGGCTTCCATAAGAAGAAATGGAGAAAATATATATAT
 ATATATATATATTGTGAAAGATCAATCCATCTGCCAGAAACTAGTGGGATGGAAGTTTGCTACAT
 GTTATCCACCCAGGCCAGGTGGAGTAACCTGAAATTATTAAAGCAGTTCTACTCAATCA
 CCAAGATGCTTCTGAAAATTGCAATTACCATTTCAACTATTTTAAAGGAAATACAGTAA
 ACATAGAGTGGTTCTCATGTGAAAATTAGCCAGCACAGATGAGCTAATTATCT
 CTTTGAGGCTCTGCTCTGTTGCTCACAGTAAACTCATTGTTAAAAGCTTCAAGAACATTCAAGC
 TGTTGGTGTGTTAAAATGCATTGATTGATTGACTGGTAGTTATGAAATTAAATTAAAACAC
 AGGCATGAATGGAAGGTGGTATTGCACAGCTAATAAATATGATTGTTGAGTATGAA

FIGURE 276

MMMVRRGLLAWISRVVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQE
EWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFL
HSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVRKDKRDELVEAIES
ALETLNNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSP
MKVKNEKLNMANTLINVIVPLAKRVDKFRQFMQNREMCIEQDGRVHLTVVYFGKEEINEVK
GILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGNSVLLFFCDVDIYFTSEFLNTCR
LNTQPGKKVFYPVLFSQYNPGIIYGHHDAVPPLLEQQLVIKKETGFWRDFGFGMTQCYRSDFI
NIGGFDLDIKGWGGEDVHLYRKYLHSNLIVVRTPVRLFHLWHEKRCMDELTPEQYKMCMQS
KAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSKKT

FIGURE 277

GAAAGAATGTTGTGGCTGCTTTTCTGGTACTGCCATTGCTGAACCTGTCAACC
AGGTGCAGAAAATGCTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAGCAT
ATGCCTGGATACCAATGAAGAATACCTCTCAAAGCGATGGTAGCTTCTCCATGAGAAAA
GTTCCCACAGAGAACAGAAATTCCATGTCCTACTTGCAATGTAACCCAGAGGGT
ATCATTCTGGTTGTGGTTACAGACCCCTCAAAAATCACACCCCTGCTGTTGAGGTGC
AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTCTTCTAAATGACCAAAC
CTGGAATTTAAAAATCCCTCCACACTGCACCACCCATGGACCCATCTGTGCCATCTG
GATTATTATTTGGTGTGATATTGCATCATCATAGTTGCAATTGCACTACTGATTAT
CAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGAT
AAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCTCTGATCCCTGGACATGAAGGG
GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGGCTCACCCCTCTGAAGGGCTGT
TGTTCTGCTTCCTCAAGAAATTAAACATTGTTCTGTGTGACTGCTGAGCATCCTGAAATA
CCAAGAGCAGATCATATATTGTTACCATTCTTTGTAATAAATTGAAATGTGCT
TGAAAGTGAAAAGCAATCAATTACCCACCAACACCACTGAAATCATAAGCTATTACGAC
TCAAAATATTCTAAAATTTCTGACAGTATAGTGTATAATGTGGTATGTGGTATTG
TAGTTATTGATTAAAGCATTAGAAATAAGATCAGGCATATGTATATATTTCACACTC
AAAGACCTAAGGAAAATAAATTCCAGTGGAGAATACATATAATATGGTAGAAATCAT
TGAAAATGGATCCTTTGACGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAG
TGAGAAGTAATTATTGTAATGGATGGATAAAATGGAATTACTCATATACAGGGTGGAAATT
TTATCCTGTTATCACACCAACAGTTGATTATATTTCTGAATATCAGCCCCTAATAGGAC
AATTCTATTGTTGACCATTCTACAATTGAAAAGTCCAATCTGTGCTAACTTAATAAAG
TAATAATCATCTTTAAAAAAAAAAAAAAAAAAAAAA

FIGURE 278

MLWLLFFLVTAIHAELCQPGAEAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVP
NCREATEISHVLLCNVTQRVSFWFVVTDPSKNHTLPAVEVQSAIRMNKNRINNAFFLNDQTL
FLKIPSTLAPPMDPSVPIIIIFGVIFCIIVATALLILSGIWQRRRKNKEPSEVDDAEDKC
ENMITIENGIPSDPLDMKGGLMMPS

FIGURE 279

AACTCAAACCTCTCTGGGAAAACGCGGTGCTGCTCCTCCGGAGTGGCCTGGCAGG
 GTGTTGGAGCCCTCGGTCTGCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTCCCTC**ATGT**
 ATGGCAAGAGCTACTCGTGCAGTGCTTCTCCTGGCATACAGCTCACAGCTCTTGG
 CCTATAGCAGCTGTGGAAATTATACCTCCCGGTGCTGGAGGCTGTTAATGGGACAGATGC
 TCGGTTAAAATGCACTTCTCCAGCTTGCCCCTGTGGGTGATGCTCTAACAGTGACCTGGA
 ATTTTCGTCCTCTAGACGGGGGACCTGAGCAGTTGTATTCTACTACCACATAGATCCCTC
 CAACCCATGAGTGGCGGTTAAGGACCGGGTGTCTGGATGGGAATCCTGAGCGGTACGA
 TGCCTCCATCCTCTGGAAACTGCAGTTGACGACAATGGGACATAACACCTGCCAGGTGA
 AGAACCCACCTGATGTTGATGGGGATAGGGGAGATCCGGCTCAGCGTCGTGACACTGTA
 CGCTTCTCTGAGATCCACTCCTGGCTCTGCCATTGGCTCTGCCTGTGCACTGATGATCAT
 AATAGTAATTGTTAGTGGCCTCTCCAGCATTACGGAAAAAGCGATGGCCGAAAGAGCTC
 ATAAAGTGGTGGAGATAAAATCAAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAGGTCTCT
 GTTTATTAGAAGACACAGAC**TAA**CAATTAGATGGAAGCTGAGATGATTCCAAGAACAA
 GAACCCTAGTATTCTGAAGTTAATGAAACTTTCTTGGCTTTCCAGTTGTGACCCGT
 TTTCCAACCAGTTGCAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCAC
 AGTGCTCCTCCATATCACCAGTCATACACAGCCTCATTATTAAGGTCTTATTAAATTCA
 GTGTAATTTCAAGTGCTCATTAGGTTATAAACACAAGAGCTACATTGGCCCTTAA
 GACACTACTTACAGTGTATGACTGTATACACATATTGGTATCAAAGGGATAAAAGCC
 ATTGTTACTCTTCCCTCCACATTCTCAATTAAAGGTGAGCTAACGCTCCTCGGTG
 TTTCTGATTAACAGTAAATCCTAAACTGTTAAATGACATTGTTATTGTC
 TCCTTAACATGAGACACATCTGTTACTGAATTCTTCAATATTCCAGGTGATAGATT
 TTTGTCG

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FIGURE 280

MYGKSSTRAVLLLLGIQLTALWPIAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALT
VNFRPLDGGPEQFVFYYHIDPFQPMGRFKDRVSDGNPERYDASILLWKLQFDDNGTYTCQ
VKNPPDVGVIGEIRLSVVHTVRFSEIHFLALAIGSACALMIIIVVVVLFQHYRKKRWAER
AHKVVEIKSKKEERLNQEKKVSVYLEDTD

FIGURE 281

GCATTTGTCTGTGCTCCCTGATCTCAGGTACCAACCATGAAGTTCTTAGCAGTCCTGGT
ACTCTTGGGAGTTCCATCTTCTGGTCTCTGCCAGAATCCGACAACAGCTGCTCCAGCTG
ACACGTATCCAGCTACTGGCCTGCTGATGATGAAGCCCCTGATGCTGAAACCAC TGCTGCT
GCAACCAC TGCGACC ACTGCTGCT CCT ACC ACTGCAACCACCGCTGCTTCTACC ACTGCTCG
TAAAGACATTCCAGTTACCCAAATGGGTTGGGGATCTCCCGAATGGTAGAGTGATGATTTC
GAGATGGAATCAGCTTGAGTCTGCAATTGGTCACAACATTGATGCTTCTGTGATTTC
ATCCAAC TACTTACCTTGCC TACGAT ATCCCTTATCTCTAATCAGTTATTTCTTCAA
ATAAAAAATAACTATGAGCAACATAAAAAAAAAAAA

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FIGURE 282

MKFLAVLVLLGVSIFLVSAQNPTTAAPADTYPATGPADDEAPDAETTAATTATTAAPTTAT
TAASTTARKDIPVLPKWVGDLPNGRVCP

FIGURE 283

GGACTCTGAAGGTCCAAGCAGCTGCTGAGGCCCAAGGAAGTGGTTCCAACCTTGGACCC
CTAGGGGTCTGGATTCGCTGGTTAACAGATAACCTGAGGGCAGGACCCATAGGGGA**ATGC**
TACCTCCTGCCCTTCCACCTGCCCTGGTGTACGGTGGCCTGGTCCCTCCTGCCGAGAGA
GTGTCTGGTCAGGGACGCAGAGGACGCTCACAGACTCCAGCCCTTGTACCGAGAGGAC
ACTTGGCAAGGTCCAGCGATGGTCCGGAGTCCACACACAGACTGGCGGCAGGGCAGGAGGGG
GACAGTTCTGTTGCTTGGTGGACAGTAAGAGGGCTTGGCCAGTCCAGGGTGGGGGCG
GCAAACCTCCATAAAGAACAGAGGGCTGGGCCACAGAGTCATCTGCCAGCTCCT
CTGCTGCTGCCAGTGGAGTGGCACGGTGGGCTTGTGCCAG**TAA**AACCACAGGCTGG
ATTGCTGCAGGCCATGGTCCCTGTCTAGGGCAGCAATTCTAACCTTGTGCTCTCAGGA
CCCCAAAGAGCTTCATTGTATCTATTGATTTCACACATTAGCAATTAAAAGTGAGAAAT
GGGCCGGGCACGGTGGCTACGCCGTAAATCCCAGCACTTGGGAGGCCGAGGCAGGGTGGAT
CACCTGAGATCAGGAGTTCAAGACCAGCCTGGCAACATGGTAAACCTTGTCTACTAAAAA
TACAAAAAAATTAGCCAGGCACAGTGGTGTGCAGTGGTAGTCCAGTTACTCGGGAGGCTGAG
GCAGGAAAATCGCTTGAACCCAGGAGGCGGACGTTGGTGGAGGCCGAGATCGCGCCGCTGAT
TCCAGCCTGGCGACAAGAGTGAGACTCCATCTCACACA

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FIGURE 284

MLPPALPPALVFTVAWSLLAERVSVRDAEDAHLQPFVTERTLGKVQRWSGVHTQTGGAG
GGQFCCAWLDSKRLASPGWGAANSIKNQRVWAPATESSAQLLCCWPVGVARGGALCQ

FIGURE 285

GTCATGCCAGTGCCTGCTCTGTGCCTGCTCTGGGCCCTGGCAATGGTGACCCGGCCTGCCTCA
GCGGCCCATGGCGGCCAGAACTGGCACAGCATGAGGAGCTGACCTGCTCTCCATGG
GACCCTGCAGCTGGGCCAGGCCCTAACGGTGTACAGGACACGGAGGGACGGCTGACAA
AGGCCAGGAACAGCCTGGGTCTCTATGCCGCACAATAGAACTCCTGGGGCAGGAGGTAGC
CGGGGCCGGGATGCAGCCCAGGAACCTCGGCAAGCCTGTTGGAGACTCAGATGGAGGAGGA
TATTCTGCAGCTGCAGGCAGAGGCCACAGCTGAGGTGCTGGGGAGGTGGCCAGGCACAGA
AGGTGCTACGGGACAGCGTGCAGCGGCTAGAAGTCCAGCTGAGGAGCGCCTGGCTGGCCCT
GCCTACCGAGAATTGAGGTCTAAAGGCTACGCTGACAAGCAGAGCCACATCCTATGGC
CCTCACAGGCCACGTGCAGCGCAGAGCGGGAGATGGTGGCACAGCAGCATCGGCTGCGAC
AGATCCAGGAGAGACTCCACACAGCGGCCTCCAGCCTGAATCTGCCTGGATGGAAC TGAG
GACCAATCATGCTGCAAGGAACACTCCACGCCCGTGAGGCCCTGTGCAGGGAGGAGCTG
CCTGTTCACTGGGATCAGCCAGGGCGCCGGCCCCACTCTGAGCACAGAGCAGAGACAGAC
GCAGGCAGGGACAAAGGCAGAGGATGTAGCCCCATTGGGGAGGGTGGAGGAAGGACATGTA
CCCTTCATGCCTACACACCCCTCATTAAAGCAGAGTCGTGGCATTCAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 286

MPVPALCLLWALAMVTRPASAAPMGGPELAQHEELLLL FHGTIQLGQALNGVYRTTEGRLLTK
ARNSLGLYGRTIELLGQEVSRRDAAQELRASLLETQMEEDILQLQAEATAEVLGEVAQAQK
VLRDSVQRLEVQLRSAWLGPAYREFEVLKAHADKQSHILWALTGHVQRQRREMVAQQHRLRQ
IQERLHTAALPA

FIGURE 287

GGCAACATGGCTCAGCAGGCTTGCCCCAGAGCCATGGCAAAGAATGGACTTGTAAATTGCAT
 CCTGGTATCACCTTACTCCTGGACCAGACCACAGCCACACATCCAGATTAAAAGCCAGGA
 AGCACAGCAAACGTCGAGTGAGAGACAAGGATGGAGATCTGAAGACTCAAATTGAAAAGCTC
 TGGACAGAACGTCAATGCCTTGAAGGAAATTCAAGCCCTGCAGACAGTCTGTCTCCGAGGCAC
 TAAAGTTACAAGAAATGCTACCTGCTCAGAAGGTTGAAGCATTCCATGAGGCCAATG
 AAGACTGCATTCCAAGGAGGAATCCTGGTTATCCCCAGGAACCTCGACGAAATCAACGCC
 CTCCAAGACTATGGTAAAGGAGCCTGCCAGGTGTCAATGACTTTGGCTGGCATCAATGA
 CATGGTCACGGAAGGCAAGTTGTTGACGTCAACGGAATCGCTATCTCCTCCTCAACTGGG
 ACCGTGCACAGCCTAACGGTGGCAAGCGAGAAAATGTGTCCTGTTCTCCAATCAGCTCAG
 GGCAAGTGGAGTGTGAGGGCTGTCGAGCAGCAAGAGATAACATATGCGAGTTACCATCCC
 TAAATAGGTCTTCTCCAATGTGTCCTCCAAGCAAGATTCACTACATAACTTATAGGTTCATGA
 TCTCTAAGATCAAGTAAAACTATAATTTTACTTATTAAAAAATTGCAACACAAGATCAAT
 GTCCATAGCAATATGATAGCATCAGCCAATTTGCTAACACACATTCTTGGGATTTGCCCT
 TCCTGGGTATAGGGATCAGAAATATTGATCCATGTGCACGCCAGATAAAATGGCTTCTGCT
 AAACAGACTAAATCTTCTCTAGTCTTCACTTAGTACAAACCCAGTTGGTTTCAAA
 AAATCACAGTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTTAGGCTACCTGAAAGATT
 TTCCCTTGGAAAGTTAGCGTATGTTGACTAACAAAAATTCCCTACATCAGAGACTCTAGGT
 GCTATATAATCCAAAAACTTTCACTGCTTCACTGCTCATTCTGCTCCATGCTGGCAATAATACC
 TTGTCAGCCCATTACCTTATTTGAATTGCTCCATCTCCTGGTGGACTTGTATCTGTCT
 GCCATATCAGAACACAAACCCCTGAAGAGGTTCTGATTGATTTTTTTCTTCATGCC
 TACCCCTTTGGAAAGTTCCAGCCGAATTGAAATGACAAGGTGTATATTGAT
 CAATTTCATTCCCACCATGCATTACAACCTCTAACATTAAATGGTAACCCATAAGGCATAT
 CAAAGAACGAGATTGCATGATAAACGGAAATAGAAAAAGAACCTACATTATTGCTTT
 AGCATCCTACTCTCACCTTATGAGATTGAGAGTGGACTTACATTCTTTTACATT
 TCGTATATTATTTTTAGCCATCATTATATGTTAAGTCTATTATGGCAACCAATCTT
 TGGAAAGCTGAAACTGAATTAAAGAATGCTATCTGGAAAATTGCATACGTCTGTGCAATT
 TTTTATTCTGCCTAGTGCTATTCTGCTTAACTAGATTGTACAAAATACTCATTGCT
 TAATATCAAATTACAAAGTTAGACTTGGAGGGAAATGGCTTTTAGAAGCAAACAATT
 AAATATATTGTTCTCAAATAATAGTGTAAACATTGAATGTGTTGTGAACAAATAT
 CCCACTTGCAAACCTTAACACATGCTTGAATTAGTTAGCTGTTTCATTGCTCA
 ATAATAAAGCCTGAATTCTGATCAATAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 288

MAQQACPRAMAKNGLVICILVITLLLQTTTSRLKARKHSKRRVRDKDGDLKTQIEKLWT
EVNALKEIQALQTVCLRGTVKHKCYLASEGLKHFEANEDCISKGGILVI PRNSDEINALQ
DYGKRSLPGVNDFWLGINDMVTEGKFVDVNGIAISFLNWDRAQPNGGKRENCVLFQSQAQGK
WSDEACRSSKRYICEFTIPK

FIGURE 289

GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTGCCCGGGCAGCCGCAGGTTCCCCGCGC
CCCGAGCCCCCGCGCC**ATGA**AAGCTCGCCGCCCTCCTGGGCTCTGCGTGGCCCTGCTGCA
GCTCCGCTGCTGCTTCTTAGTGGGCTCGCCAAGCCTGTGGCCAGCCTGTCGCTGCGCTG
GAGTCGGCGGCGAGGCCGGGACCCCTGGCAACCCCTCGCACCCCTAACCCGCT
GAAGCTCCTGCTGAGCAGCCTGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGT
GTGTGGCTGAGCTGGTCCCCAGGCCGTGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGG
GCCCTGACAGTGGT**TGA**GCCGAGACTGGAGCATCTACACCTGAGGACAAGACGCTGCC
CACCCCGAGGGCTGAAACCCCGCCGCGGGGAGGACCGTCCATCCCCCTCCCCCGGCCCT
CTCAATAAACGTGGTTAAGAGCAAAAAAAAAAAAAAAA
AAAAAAAAAAAAA

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FIGURE 290

MKLAALLGLCVALSCSSAAFLVGSAKPVAQPVALESAAEAGAGTLANPLGTLNPLKLLS
SLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTIVFG

FIGURE 291

FIGURE 292

MKVVPULLSVLLAQVWLVPGAPSPQSPETPAPQNQTSRVVQAPREEEDEQEASEEKAGE
EEKAWLMASRQQQLAKETSNGFSLLRKISMHDGNMVFSPFGMSLAMTGLMLGATGPTETQI
KRGHLHQALKPTKPGLLPSLFKGRLRETLSRNLELGLSQGSFAFIHKDFDVKETFFNLSKRYF
DTECVPMNFRNASQAKRLMNHYINKETRGKIPKLFDEINPETKLILVDYILFKGKWLTDFDP
VFTEVDTFHLDKYKTIKVPMMYGAGKFASTFDKNFRCHVLKL PYQGNATMLVVLMEMGDHL
ALEDYLTDLVETWLRNMKTRNMEVFFPKFKLDQKYEMHELLRQMGIRRIIFSPFADLSELSA
TGRNLQVSRLRRTVIEVDERGTEAVAGILSEITAYSMPPVIKVDRPFHFMIFYEETSGMLLF
LGRVVNPPLL

FIGURE 293

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTACAGAGACGCGGACCCCAGACATGAG
GAGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGTGGGAGGCAGGTGCAGTCCCAG
CACCCAAGGTCCCTATCAAGATGCAAGTCAAACACTGCCCTCAGAGCAGGACCCAGAGAAG
GCCTGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGCTGTTCCC
TGTCCAGAAGCCGAAACTCTTGACCACCGAGGAGAACGCCACGAGGTCAAGGCAGGGCAGGGGCC
TCCTTCCAGGCACCAAGGCCTGGATGGAGACCGAGGACACCCCTGGCCGTGTCCGTGAGTCCC
GAGCCCGACCATGACAGCCTGTACCAACCTCCGCCTGAGGAGGACCAGGGCGAGGAGAGGCC
CCGGTTGTGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGGAGGAAGACCAAGACCACA
TCTACCACCCCCAGTAGGGCTCCAGGGCCATCACTGCCCTGCCCCCTGTCCAAGGCCAGG
CTGTTGGGACTGGGACCCCTCCCTACCCCTGCCAGCTAGACAAATAACCCAGCAGGCAA
AAAAAAAAAAAAAAA

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FIGURE 294

MRRLLLVTSLVVVLLWEAGAVPAPKVPIKMQVKHWPSEQDPEKA
WGVVEPPEKDDQLVVL
FPVQKPKLLTTEEKPRGQGRGPILPGTKAWMETEDTLGRVLSPEPDHDSLYHPP
PEEDQGEE
RPRLWVMPNHQVLLGPEEDQDHIIYHPQ

FIGURE 295

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGTGAAGGAGCTCTCTG
TACCCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACA**ATG**AACCAACTCAGCTTCCTGC
TGTTTCTCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAA
TGGACCTGTTCTCGTCTCCATCTCTGCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCC
TAGTGCATTTGATGGCCTGTATTTCTCCGACTGAGAATGGTGTATCTACCAGACCTTCT
GTGACATGACCTCTGGGGTGGCGGCTGGACCCCTGGTGGCCAGCGTGCATGAGAATGACATG
CGTGGGAAGTGCACGGTGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCC
AGAGGGGACGGCAACTGGGCCAACTACAACACCTTGGATCTGCAGAGGCGGCCACGAGCG
ATGACTACAAGAACCCCTGGCTACTACGACATCCAGGCCAAGGACCTGGCATCTGGCACGTG
CCCAATAAGTCCCCCATGCAGCACTGGAGAAACAGCTCCCTGCTGAGGTACCGCACGGACAC
TGGCTTCCTCCAGACACTGGACATAATCTGTTGGCATCTACCAGAAATATCCAGTGAAAT
ATGGAGAAGGAAAGTGTGGACTGACAACGGCCCGGTGATCCCTGTGGTCTATGATTTGGC
GACGCCAGAAAACAGCATCTTATTACTCACCTATGCCAGCGGGATTCACTGCAGGGATT
TGTCAGTTCAAGGTATTAATAACGAGAGAGCAGCCAACGCCCTGTGTGCTGGAATGAGGG
TCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAGATACTTCCAGAGGCCAGT
CCCCAGCAGTGTGGAGATTTCTGGTTTGATTGGAGTGGATATGGAACTCATGTTGGTTA
CAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTCTATTCTATCGT**TGA**GAGTTTGTG
GGAGGGAAACCCAGACCTCTCCTCCACCAGAGATCCCAAGGATGGAGAACAACTACCCA
GTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAATCATATTGACTCAAGAAAAAAA

FIGURE 296

MNQLSFLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTEN
GVIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRSSQQGSKADYPEGDGNWANYNTFG
SAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLRYRTDTGFLQTLGHNLFGI
YQKYPVKYGECKCWTDNGPVIKVYDFGDAQKTASYSPYQREFTAGFVQFRVFNNERAAN
ALCAGMRVTGCNTEHHCIGGGYFPEASPQQCGDFSGFDWSGYGTHVGYSSSREITEAAVLL
FYR

FIGURE 297

GC GGAGCCGGCGCCGGCTGCGCAGAGGAGCCGCTCTGCCGCCACCTCGGCTGGGAGCC
CACGAGGCTGCCGCATCCTGCCCTCGGAACA**ATG**GGACTCGGCGCGAGGTGCTTGGGCG
CGCTGCTCCTGGGGACGCTGCAGGTGCTAGCGCTGCTGGGGCCGCCATGAAAGCGCAGCC
ATGGCGGCATCTGCAAACATAGAGAATTCTGGGCTTCCACACAACACTCCAGTGCTAACTCAAC
AGAGACTCTCAAACATGTGCCTCTGACCATAACAAATGAAACCTCCAACAGTACTGTGAAAC
CACCAACTTCAGTTGCCTCAGACTCCAGTAATAACACGGTCACCACCATGAAACCTACAGCG
GCATCTAATAACAACACCAGGGATGGTCTAACAAATATGACTTCTACCACCTAAAGTC
TACACCCAAAACAACAAGTGTTCACAGAACACATCTCAGATATCAACATCCACAATGACCG
TAACCCACAATAGTCAGTGACATCTGCTGTTCATCAGTAACAATCACAACAATATGCAT
TCTGAAGCAAAGAAAGGATCAAAATTGATACTGGGAGCTTGGTATTGTATTAAAC
GCTGGAGTTTATCTATTCTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATTC
GGTATCGAACCATAGATGAACATGATGCCATCATT**TAA**GGAAATCCATGGACCAAGGATGGA
ATACAGATTGATGCTGCCCTATCAATTAAATTGGTTATTAATAGTTAAAACAATATTCT
CTTTTGAAAATAGTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAAATATGTA
AAGATTCTCAAGGTAACAAGGGTTGGGTTGAAATAACATCTGGATCTTATAGACCGT
TCATACAATGGTTTAGCAAGTTCATAGTAAGACAAACAAGTCCTATCTTTGGCT
GGGGTGGGGCATTGGTCACATATGACCAGTAATTGAAAGACGTCACTGAAAGACAGAA
TGCCATCTGGGCATACAAATAAGAAGTGTACAGCACTCAGGATTTGGTATCTTGT
AGCTCACATAAGAACCTCAGTGCTTTCAGAGCTGGATATCTTAATTACTAATGCCACA
CAGAAATTATAACAATCAAACATAGATCTGAAGCATAATTAAAGAAAAACATCAACATTGG
TGCTTTAAACTGTAGTAGTTGGTCTAGAAACAAAATCTCC

FIGURE 298

MGLGARGAWAALLLGTIQLVALLGAAHESAAMAASANIENSGLPHNSSANSTETLQHVPSDH
TNETSNSTVKPPTSVASDSSNTTVTTMKPTAASNTTPGMVSTNMTSTTLKSTPKTTSVSQN
TSQISTSTMVTNHNSVTSAASSVTITTMHSEAKKGSKFDTGSFVGGIVLTLGVLSILYIG
CKMYYSRRGIRYRTIDEHDAAII

FIGURE 299

CAGCCGGGTCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCGAGCCGGAGCCGG
 TCGCGGGGGCTCCGGCTGTGGACCGCTGGCCCCAGCG**ATG**GCGACCCTGTGGGAGGC
 CTTCTCGGCTTGGCTCCTGCTCAGCCTGTCGTGCCTGGCGCTTCCGTGCTGCTGCC
 GCAGCTGTCAGACGCCAAGAATTGAGGATGTCAGATGTAATGTATCTGCCCTCC
 ATAAAGAAAATTCTGGGCATATTATAAAGAACATATCTCAGAAAGATTGTGATTGCC
 CATGTTGTGGAGCCATGCCTGTGCGGGGGCTGATGTAGAACATACTGTCTACGCTGTGA
 ATGCAAATATGAAGAAAGAACAGCTCTGTACAATCAAGGTTACCATATAATTATCTCTCCA
 TTTTGGCCTTACTTCTGTACATGGTATATCTTACTCTGGTGAGCCCATACTGAAGAGG
 CGCCTCTTGGACATGCACAGTTGATAACAGAGTGTGATATTGGGATCACCAGCCTT
 TGCAAATGCACACGATGTGCTAGCCGCTCCGCAGTCGAGCCAACGTGCTGAACAAGGTAG
 AATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTGACCGG
 CATGTTGCCTCAG**TAA**TTGGGAATTGAATTCAAGGTGACTAGAAAGAACAGGCAGACAA
 CTGGAAAGAACTGACTGGGTTTGCTGGTTCATTTAACCTTGTGATTTCACCAACT
 GTTGCTGGAAGATTCAAAACTGGAAGCAGAAAACTTGCTGATTTTTCTTGTAAACGTA
 ATAATAGAGACATTTAAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTCCCTATTG
 TGACTTTACTAATAAAAATCTGCCTGAAATTATCTTGAAGTCCTTACCTGGAACA
 AGCACTCTTTTACCATAGTTAACCTGACTTCAAGATAATTTCAGGGTTTG
 TTGTTGTTGTTTGTGTTGGTGGAGAGGGGAGGGATGCCTGGAAAGTGGTT
 AACAACTTTTCAAGTCACTTACTAAACAAACTTTGTAATAGACCTTACCTTCTATT
 TCGAGTTCAATTATATTGCACTGTATTATCTGGGTATCTGCTGTGCTGCACCTCATGGTAAACGGGAT
 CTAAAATGCCTGGTGGCTTCAAAAAAGCAGATTTCATGTAAGTGTGATGTCTGATG
 CAATGCATCCTAGAACAAACTGCCATTGCTAGTTACTCTAAAGACTAAACATAGTCTG
 GTGTGTGTGGTCTTACTCATCTTAGTACCTTAAGGACAAATCTAAGGACTTGGACACT
 TGCAATAAGAAATTATTTAAACCAAGCCTCCCTGGATTGATAATATACACATTG
 TCAGCATTCCGGTGTGGTGGAGAGGCAGCTGTTGAGCTCCAATATGTGCAGCTTGA
 AGGGCTGGGTTGTGGTGCCTCTGAAAGGTCTAACCATATTGGATAACTGGCTTT
 TCTTCATGTCCCTTTGAAATGTAACAATAAAATAATTGAAACATCAA

300/330

FIGURE 300

MATLWGGLLRLGSLLSCLALSVILLALAQLSDAAKNFEDVRCKCICPPYKENSIGHYNKNIS
QKDCDCLHVVEPMPVRGPDVEAYCLRCECKYEERSSVTIKVTIIYLSILGLLLLYMVYLT
VEPILKRRLFGHAQLIQSDDDIGDHQPFANAHDVLRARSRSRANVLNKVEYAQQQRWKLQVQE
RKSVFDRHVVLS

FIGURE 301

GCACCTGCGACCACCGTGAGCAGTCATGCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTT
CTGGGCTTGTCTGGCTCTGTCGCTGCTGCCAAGGCCTCCTGTCCCAGGGAAAGCGG
CAGGAGCCGCCGCGACACCTGAAGGAAAATTGGGCCGATTCCACCTATGATGCATCATCA
CCAGGCACCCCTCAGATGGCCAGACTCCTGGGGCTCGTTCCAGAGGTCTCACCTGCCGAGG
CATTGCAAAGGCCAAGGATCAGGTGGAGGTGCTGGAGGAGGGTAGTGGAAAGAGGTCTG
ATGGGGCAGATTATTCCAATCTACGGTTTGGGATTTTATATATACTGTACATTCTATT
TAAGGTAAGTAGAATCATCCTAACATATTACATCAATGAAAATCTAATATGGCGATAAAAA
TCATTGTCTACATTAACCTCTTATAGTTCATAAAATTATTCAAATCCATCATCTCTTA
AATCCTGCCTCCTCTCATGAGGTACTTAGGATAGCCATTATTCAGTTCACATAAGAATG
TTTACTCAATGTTAAGTGTGCCCCAAATTACAACAAACAAGGCAGAACTAGGACTT
GAACATGGATCTTGGTTCTTAATCCAGTGAGTGATACAATTCAATGCACTCCCTGCCA

FIGURE 302

MAYSTVQRVALASGLVLALSLLLPKAFLSRGKRQEPPPTPEGKLGRFPPMMHHQAPSDGQT
PGARFQRSHLAEAFAKAKGSGGAGGGSGRGLMGQIPIYGFYIFLYILFKVSRIILI
ILHQ

FIGURE 303

CGGCTCGAGTGCAGCTGTGGGAGATTCACTGCATTGCCCTGGGTGCTCTTCATCTT
 GGATTGAAAGTTGAGAGCAGC**ATG**TTTGCCCCTGAAACTCATCCTGCTGCCAGTGTAC
 TGGATTATTCCCTGGGCCTGAATGACTTGAATGTTCCCCGCTGAGCTAACAGTCCATGTG
 GGTGATTCACTGCTGATGGATGTGTTCCAGAGCACAGAAGACAAATGTATATTCAAGAT
 AGACTGGACTCTGTCACCAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTCTCA
 ATCTCAGTGTGCCTATTGGCGCTTCCAGAACCGCGTACACTGATGGGGACATCTTATGC
 AATGATGGCTCTCCTGCTCCAAGATGTGCAAGAGGGCTGACCAGGAACCTATATCTGTGA
 AATCCGCCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCAGGTGACTGCATGTGCTTCCAG
 AGGAGCCCAAAGAGCTCATGGTCCATGTGGGTGGATTGATTCAAGATGGATGTGTTCCAG
 AGCACAGAAGTGAAACACGTGACCAAGGTAAGATGGATATTCAGGACGGCGCGCAAAGGA
 GGAGATTGTATTCGTTACTACCACAAACTCAGGATGTCTGTGGACTACTCCCAGAGCTGGG
 GCCACTCCAGAACATCGTGTGAACCTGGTGGGGACATTTCCGCAATGACGGTTCCATCATG
 CTTCAAGGAGTGAGGGAGTCAGATGGAGGAAACTACACCTGCAGTATCCACCTAGGGAACCT
 GGTGTTCAAGAAAACCATTGTGCTGCATGTCAGCCCCGAAGAGCCTCGAACACTGGTACCC
 CGGCAGCCCTGAGGCCTCTGGTCTGGTGGTAATCAGTTGGTGTGACATTGTGGAAATTGTC
 TGTGCCACAATCCTGCTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAAATAA
 GAGTTCAAGTGAATTCTACAGTCTGGTGAAGAACACGAAGAAGACTAACAGAGATAAAAG
 AAAAACCTGCCATTGAAAGATGTGAAGGGGAGAAACACATTTACTCCCCATAATTGTA
 CGGGAGGTGATCGAGGAAGAACCAAGTGAAAATCAGAGGCCACCTACATGACCATGCA
 CCCAGTTGGCCTCTGAGGTCAAGTCGAACAACTCACTGAAAAAAAGTCAGGTGGGG
 GAATGCCAAAAACACAGCAAGCCTT**TGA**GAAGAATGGAGAGTCCCTCATCTCAGCAGCGG
 TGGAGACTCTCCTGTGTGTCTGGGCCACTCTACAGTGATTCAGACTCCGCTCTC
 CCAGCTGTCCTCCTGTCATTGTTGGTCAATACACTGAAGATGGAGAATTGGAGCCTGG
 CAGAGAGACTGGACAGCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGC
 CTCTGGAGTGGACACTGGCCCTGGAACCCAGGCTGAGCTGAGTGGCCTCAAACCCCCCGTT
 GGATCAGACCCCTCTGTGGCAGGGTTCTAGTGGATGAGTTACTGGGAAGAATCAGAGATA
 AAAACCAACCCAAATCAA

FIGURE 304

MFCPLKLILLPVLLDYSLGLNDLNVSPPLETvhVGDSALMGCVFQSTEDKCIFKIDWTLS
PG
EHAKDEYVLYYSNLSPVIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYICEIRLK
GES
QVFKKAVVLHVLPEEPKELMVHGGLIQMGCVFQSTEVKHVTKVEWIFSGRR
AKEEIVFRYY
HKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDG
GNYTC
SIHLGNLVFKKTIV
LHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLPVLILIVKKTC
GNKSSVN
STV
LVKNTKTNPEIKEKPCHFERCEGEKHIYSPIIVREVIEEE
PSEKSEATYMTMHPVWPSLR
SDRNNNSLEKKSGGGMPKTQQAF

FIGURE 305

CTATGAAGAAGCTCCTGGAAAACAATAAGCAAAGGAAACAAATGTGTCCCATCTCACATG
GTTCTACCCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATTGTAAGAGTTGG
AAACTACATTTGCAAAGTCATTGAACCTGAGCTCAGTGCAGTACTCGGGAAAGCC**ATGCA**
GGATGAAGATGGATACATCACCTTAAATATTAAAACCGGAAACCAGCTCTCGTCTCCGTTG
GCCCTGCATCCTCCTGGTGGCGTGTGATGGCTTGATTCTGCTGATCCTGTGCGTGGGG
ATGGTTGTCGGGCTGGTGGCTCTGGGATTTGGTCTGTCATGCAGCGCAATTACCTACAAGA
TGAGAATGAAAATCGCACAGGAACCTGCAACAATTAGCAAAGCGTTCTGTCAATATGTGG
TAAAACAATCAGAACTAAAGGGACTTCAAAGGTATAATGCAGCCCCGTGACACAAAC
TGGAGATATTATGGAGATAGCTGCTATGGTTCTCAGGCACAACCTAACATGGGAAGAGAG
TAAGCAGTACTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGG
AGTACATCAAAGCCAGGACTCATTAAATTGTTGGTCGGATTATCTGCCAGAAGTCGAAT
GAGGTCTGGAAGTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTGAGTTTGGAAAGA
TGGAAAAGGAAATATGAATTGTGCTTATTTCATAAATGGAAAATGCACCCACCTCTGTG
AGAACAAACATTATTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCT
TAATGCAAAGAGGTGGACAGGATAACACAGATAAGGGCTTATTGTACAATAAAAGATATGT
ATGAATGCATCAGTAGCTGAAAAAAAAAAAAAA

FIGURE 306

MQDEDGYITNIKTRKPALSVGPASSSSWRVMALILLILCVGMVGLVALGIWSVMQRNYL
QDENENRTGTLQQLAKRFCQYVVVKQSELKGTFKGHKCSPCDTNWRYYGDSCYGF
FRHNLTWE
ESKQYCTDMNATLLKIDNRNIVEYIKARTHLLRWVGLSRQKSNEVWK
WEDGSVISENMF
EDGKGNNMCAYFHNGKMHPTFCENKH
YLMCERKAGMTKVDQLP

FIGURE 307

CCCACGCGTCCGCGCAGTCGCGCAGTTCTGCCTCCGCCTGCCAGTCTGCCCGCGATCCGG
 CCCGGGGCTGTGGCGTCGACTCCGACCCAGGCAGGCCAGCAGCCCCGCGCGGGAGCCGGACCGC
 CGCCGGAGGAGCTGGACGGCATGCTGAGCCCCCTCCTTGCTGAAGCCCAGTGCAGAAGAA
 GCCCGGGCAAACGCAGGCTAAGGAGACCAAAGCGGCGAAGTCGCGAGACAGCGGACAAGCAG
 CGGAGGAGAAGGAGGAGGAGGCGAACCCAGAGAGGGCAGCAAAAGAAGCGGTGGTGGTGG
 CGTCGTGGCC**ATG**CGGGCGGCTATGCCAGCTCGCTCATCCGTAGAACAGAGGCAAGCCCGCG
 AGCGCGAGAAATCCAACGCCCTGCAAGTGTGTCAGCAGCCCCAGCAAAGGCAAGACCAGCTGC
 GACAAAAACAAGTTAAATGTCTTTCCCGGGTCAAACCTTCGGCTCCAAGAACAGGCGCAG
 AAGAACGACAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATAACAGCCGACAAGGCTACC
 ACTTGCAGCTGCAGGCAGGATGGAACCATTGATGGCACCAAAGATGAGGACAGCACTTACACT
 CTGTTAACCTCATCCCTGTGGGTCTGCGAGTGGTGCTATCCAAGGAGTTCAAACCAAGCT
 GTACTTGGCAATGAACAGTGAGGGATACTTGTACACCTCGGAACCTTCACACCTGAGTGCA
 ATTCAAAGAACATCAGTGTGAAAATTATTATGTGACATATTCAATGATATAACGTCAG
 CAGCAGTCAGGCCAGGGTGGTATCTGGGTCTGAACAAAGAACAGGAGAGATCATGAAAGGCAA
 CCATGTGAAGAACACAAGCCTGCAGCTATTCCTGCCTAAACCAACTGAAAGTGGCCATGT
 ACAAGGAGCCATCACTGCACGATCTCACGGAGTTCTCCGATCTGGAAAGCGGGACCCCAACC
 AAGAGCAGAAGTGTCTGGCGTGCTGAACGGAGGCAAATCCATGAGCCACAATGAATCAAC
G**TAG**CCAGTGAGGGCAAAGAACAGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAAT
 TCTTCTAGCAGTCCTTCACCCAAAAGTTCAAATTGTCAGTGACATTACCAAACAAACAGG
 CAGAGTTCACTATTCTATGCCATTAGACCTTCTTATCATCCATACTAAAGC

FIGURE 308

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498
><subunit 1 of 1, 245 aa, 1 stop
><MW: 27564, pI: 10.18, NX(S/T): 1
MAAAIASLIRQKRQAREREKSACKCVSSPSKGKTSCDKNKLNVFSRVKLFGSKKRRRRP
EPQLKGIVTKLYSRQGYHLQLQADGTIDGKDEDSTYTLFNLIPVGLRVVAIQGVQTKLYLA
MNSEGYYLTSELFPECKFKESVFENYYVTYSSMIYRQQQSGRGWYLGLNKEGEIMKGNHVK
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPKSRSVSGVLNGGKSMHNEST
```

N-glycosylation site.

amino acids 242-246

Glycosaminoglycan attachment site.

amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site.

amino acids 93-100

N-myristoylation site.

amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop).

amino acids 231-239

HBGF/FGF family proteins

amino acids 78-94, 102-153

FIGURE 309

CCAGGATGGAGCTGGGCCTGTATGCCATTATTGTTCTATGCTACTAGACATGGGGGG
 ACTTGGTGAAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTACTGAACCTGGG
 CAACCTGGATATTCTGAGACATATTGGGGGATTCAGTAAAAAGTGGGGATCCCCT
 CCATTTAGAGTGTAGCAAAGGAAAAACACCAAGGTTGGGTCCTCCTGACATTGGCAGTG
 CCCCAGTAGGGTGGGATGAGCGAATATTCCAAAGCTAAAGTCCCACACCCTGTAGATTAC
 AAGAGTGGATTGGCAGGAGTGTGCCAAAATACAGTGGAAAGGTGCCTGAAGATAATTAA
 ACCACGTCTGGAAATTAGTGGTCTTGGCTTGGATAGGTGAAGTGAGGACAGACACTG
 GAGAGGAGGGAAAGGGACGTTTCAATAGGAGGCACGACTGGGCCACGGTGGTAAGTGGCTGCT
 AGTACATAGGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCACGGTGGTAAGTGGCTGCT
 GTGGAGGGGGTACGTGAGGGGGGCTGGGCTTACCTCAGGTCCGTGGGTGGGCAG
 CGAGTCGGGCCTGAGCGTAAGAGCATGCCCTAGTGAGCGGCCCTCTGGGGAGGCCAG
 CGCGCTCCGGCGCCTGCCGTTGGGGTGTCTCCCTCCCGGGCGCT**ATG**GCGGCGCTGGC
 CAGTAGCCTGATCCGGCAGAACGGAGGTCCCGAGCCCCGGGGCAGCCGGCGTGTGG
 CGCAGCGCGCGTGTGTCCCGCGCACCAAGTCCCTTGCCAGAACAGCTCCTCATCCTG
 CTGTCCAAGGTGCGACTGTGCGGGGGCGGCCGCGCCGGACCGCGGCCGGAGCCTCA
 GCTCAAAGGCATCGTACCAAAACTGTTCTGCCGCCAGGGTTCTACCTCCAGGCGAATCCCG
 ACGGAAGCATCCAGGGCACCCAGAGGATACCAGCTCCTCACCCACTCAACCTGATCCCT
 GTGGGCCTCCGTGGTCAACATCCAGAGGCCAACGCTGGTCACTACATGGCATGAATGC
 TGAGGGACTGCTCTACAGTCGCCGCATTACAGCTGAGTGTGCTTAAGGAGTGTGTCT
 TTGAGAATTACTACGTCCGTACGCCCTGCTCTACCGCCAGCGTCGTTCTGGCCGGGCC
 TGGTACCTCGGCCTGGACAAGGAGGGCCAGGTCAAGGGAAACCGAGGTTAAGAAGACCAA
 GGCAAGCTGCCACTTCTGCCAACGCTCCTGGAGGTGCCATGTACCAGGAGCCTCTCC
 ACAGTGTCCCCGAGGCCTCCCTCCAGTCCCCCTGCC**TGA**AATGTAGTCCCTGGACTG
 GAGGTTCCCTGCACTCCAGTGAGCCAGCCACCACCAACCTGT

FIGURE 310

MAALASSLIRQKREVREPAGGSRPVSAQRRCPRGKSLCQKQLLILSKVRLCGGRPARPDR
GPEPQLKGIVTKLFCRQGFYLQANPDGSIQGTPEDTSSFTHFNLIPVGLRVVTIQSAKLGHY
MAMNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRRSGRAWYLGLDKEGQVMKGNR
VKKTAAAHFLPKLLEVAMYQEPLHHSVPEASPSSPPAP

Tyrosine kinase phosphorylation site:

amino acids 199-207

N-myristoylation sites:

amino acids 54-60, 89-95, 131-137

HBGF/FGF family signature:

amino acids 131-155

FIGURE 311

ATGGCCGCCCATCGCTAGCGGTTGATCCGCCAGAACGGCAGGCAGGGAGCAGCACTGGACCGGGCTCTGCAACGGCACACCTGGTGGATATCTTCTCAAAGTGCGCATCTCGGCCTCAAGAACGGCTACTACTCGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGAAGGCTACTACTGCAAATGCACCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCTCAACCTCATACCAGTGGACTACGTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTATAAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTACCCCTGAATGCAAGTTTAAAGAATCTGTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGGAATCTGGTAGAGCCTGGTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGAGTAAAGAAAACCAAAACCAGCAGCTCATTCTACCCAAAGCCATTGGAAGTTGCCATGTACCGAGAACCATCTTGCATGATGTTGGGAAACGGTCCCGAAGCCTGGGTGACGCCAAGTAAAAGCACAAGTGCCTGCAATAATGAATGGAGGCAAACCAGTCACAAAGAGTAAGACAACAT**TAG**

FIGURE 312

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503
><subunit 1 of 1, 247 aa, 1 stop
><MW: 27702, pI: 10.36, NX(S/T): 2
MAAAIASGLIRQKRQAREQHWDRPSASRRRSPSKNRGLCNGNLVDIFSKVRI FGLKKRRLR
RQDPQLKGIVTRLYCRQGYYLQMHPDGALDGTKDDSTNSTLFNLI PVGLRVVAIQGVKTGLY
IAMNGEGLYLPSELFPECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR
VKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASA IMNGGKPVNKS KTT
```

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins.

amino acids 104-155, 171-198

FIGURE 313

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTGGTGGTGGCTGTTGGGTGCCTGCACAAAT
 GAAGGATGCAGGACGCAGCTTCCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGA
 ACGAACGCTTTCTTGTGAGCCCTGGATCTAACACAATGTATATGTGCACACAGGGAGCATTCAAGAATG
 AAATAAACAGAGTTAGACCCGGGGGTGGTGTGGTCTGACATAAATAATCTAAAGCAGCTGTTCCC
 CTCCCCACCCCCAAAAAAAAGGATGATTGAAATGAAGAACCGAGGATTCAAAGAAAAAGTATGTTCATTT
 TTCTCTATAAAAGGAGAAAGTGAGCCAAGGGAGATATTTGGAATGAAAAGTTGGGGCTTTTAGTAAAGTAA
 AGAACTGGTGTGGTGTGTTCTTCTTGAATTCCCACAAGAGGAGGAAATTAAATAACATCTGC
 AAAGAAATTTCAGAGAAGAAAAGTGACCGCGCAGATTGAGGCATTGATTGGGGAGAGAAACCAGCAGAGCA
 CAGTTGGATTGTGCCTATGTTGACTAAAATTGACGATAATTGCAAGTTGGATTCTTCATCAACCTCCTT
 TTTTAAATTTTATCCTTTGGTATCAAGATCATGCGTTCTTGTCTTAACCACCTGGATTCCATCT
 GGATGTTGCTGTGATCAGTCTGAAATACAACACTGTTGAATTCCAGAACGGACCAACACCAGATAAATTATGA**ATG**
 TTGAACAAGATGACCTTACATCCACAGCAGATAATGATAGGTCTAGGTTAACAGGCCCTATTGACCCCT
 GCTTGTGGTGTGCTGGCTCTTCAACTTCTTGTGGTGTGGCTGGTGTGGCGGGCTCAGACCTGCCCTGTGT
 GCTCCTGCAGCAACCAAGTCAGCAAGGTGATTGTGTCGGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCC
 ACCAACACACGGCTGCTGAACCTCCATGAGAACCAATCCAGATCATCAAAGTGAACAGCTCAAGCACTTGAG
 GCACCTGAAATCCTACAGTTGAGTAGAACCATATCAGAACCATGAAATTGGGCTTCAATGGTCTGGCGA
 ACCTCAACACTCTGAAACTCTTGACAATCGTCTTACTACCATCCGAATGGAGCTTGTATACTGTCTAAA
 CTGAAGGAGCTCTGGTGCAGAACACCCCCATTGAAAGCATCCCTCTTATGCTTTAACAGAACCTCTTCTT
 GCGCCGACTAGACTTAGGGAAATTGAAAAGACTTTCATACATCTCAGAACGGTGCCTTGAAGGCTGTCCAAC
 TGAGGTATTGAAACCTTGCATGTGCAACCTCGGAAATCCCTAACCTCACACCGCTCATAAAACATAGATGAG
 CTGGATCTTCTGGAAATCATTATGCCATCAGGCCTGGCTTTCCAGGGTTGATGCACCTCAAAACT
 GTGGATGATACAGTCCCAGATTCAAGTGATTGAACGAAATGCCCTGACAACCTCAGTCAGTGAGATCA
 ACCTGGCACACAATAATCTAACATTACTGCCATGACCTCTTCACTCCCTGCATCATCTAGAGCGGATACAT
 TTACATCACACCCCTGAACTGTAACGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTC
 GAACACAGCTTGTGCCCCGGTGTAAACACTCCCTCCAACTCAAAGGGGAGGTACATTGGAGAGCTGACCAGA
 ATTACTCACATGCTATGCTCCGGTATTGTGGAGCCCCCTGAGACCTCAATGTCAGTGAAAGGCATGGCAGCT
 GAGCTGAAATGTCGGCCTCCACATCCCTGACATCTGTATCTGGATTACTCCAAATGTAACGTGCAAGATA
 TGGGGCGTACAAAGTGGGATAGCTGTGCTCAGTGATGGTACGTTAAATTCAAAATGTAACGTGCAAGATA
 CAGGCATGTACACATGTATGGTGAGTAATTGGTGGGAAACTACTGCTCAGCCACCTGAATGTTACTGCA
 GCAACCAACTACTCCTTCTCTTCAACCGTACAGTAGAGACTATGAAACCGTCTCAGGATGGCAGCG
 GACCACAGATAACATGGGTCCCACCTCCAGTGGCGACTGGGAGACCACCAATGTGACCACCTCTCACAC
 CACAGAGCACAAGGTCGACAGAGAAAACCTTCACCATCCCAGTGACTGATATAAACAGTGGATCCCAGGAATT
 GATGAGGTGATGAAGACTACCAAAATCATCATTGGGTGTTTGTGGCATCACACTCATGGCTGCAGTGATGCT
 GGTCAATTCTACAAGATGAGGAAGCAGCACCATGGCAAAACCATCACGCCCAACAAGGACTGTTGAAATT
 TTAATGTGGATGATGAGATTACGGGAGACACACCCATGGAAAGCCACCTGCCATGCCATGCTGATCGAGCATGAG
 CACCTAAATCACTATAACTCATACAAATCTCCCTCAACCACACAACAGTTAACACAATAATTCAATACA
 CAGTTCACTGCATGAACCGTTATTGATCCGAATGAACTCTAAAGACAATGTACAAGAGACTCAAATC**TAA**AACA
 TTTACAGAGTTACAAAAACAAATCAAAAAAAAGACAGTTATTAAAAATGACACAAATGACTGGCTAA
 ATCTACTGTTCAAAAAAGTGTCTTACAAAAAAACAAAAAGAAAATTATTAAATTCTATTG
 TGATCTAAAGCAGACAAAAA

FIGURE 314

MLNKMTLHPQQIMIGPRFNRALFDPLLVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGISTNTRLLNLHENQIQIICKVNSFKHLRHEILQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHHNPWNCNCIDIL
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNTEGMAAE
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTQDTGMYTCMVSNSVGN
TTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQ
STRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
HHAPTRTVEIINVDEITGDTPMESHPMPAIEHEHLHYNSYKSPFNHTTVNTINSIHSS
VHEPLLIRMN SKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419,
434-438, 442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 315

GCGCCGGGAGCCCACCTGCCCCAGGGCACGGGGCGGGGCGCCGGCTCCGCCGGCACAT
 GGCTGCAGCCACCTCGCGCGCACCCCGAGGGCGCCGCCAGCTCGCCCGAGGTCCGTGGA
 GGCGCCCGGCCGCCCGAGCCAAGCAGCAACTGAGCGGGGAAGCGCCCGCGTCGGGATC
GGGATGTCCCTCCCTCTCTGCTAGTTCTACTATGTTGAAACCTTGGGACTCA
 CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACTTGCCTGCCACCATACTGGGGC
 TTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCGATAATGAAGGAAACCAAAA
 GTGGTGATCACTTACTCCAGTCGTATGTCTACAATAACTTGACTGAGGAACAGAAGGGCCG
 AGTGGCCTTGCTCCAATTCTGGCAGGAGATGCCTCCTGCAGATTGAACCTCTGAAGC
 CCAGTGATGAGGCCGGTACACCTGTAAGGTAAGAATTCAAGGGCGCTACGTGAGGAGCCAT
 GTCATCTAAAAGTCTTAGTGAGACCATCCAAGCCAAGTGTGAGTTGAAAGGAGAGCTGAC
 AGAAGGAAGTGAACCTGACTTTGCACTGTGAGTCATCCTCTGGCACAGAGGCCATTGTATT
 ACTGGCAGCGAACCGAGAGAAAAGAGGGAGAGGATGAACGTCGCTGCCCTCCAAACTTAGGATT
 GACTACAACCACCCCTGGACGAGTTCTGCTGCAAGATCTTACCATGTCCTACTCTGGACTGTA
 CCAGTGACAGCAGGAACGAAGCTGGAAAGGAAAGCTGTGTTGCGAGTAACGTACAGT
 ATGTACAAAGCATCGGCATGGTGAGGAGCAGTGACAGGCATAGTGGCTGGAGGCCCTGCTG
 ATTTCCTCTGGTGTGGCTGCTAATCGAAGGAAAGACAAAGAAAGATATGAGGAAGAAGA
 GAGACCTAATGAAATTGAGAAGATGCTGAAGCTCCAAAAGCCGTCTGTGAAACCCAGCT
 CCTCTCCTCAGGCTCTGGAGCTACGCTCTGGTTCTCCTCCACTCGCTCCACAGCAAAT
 AGTGCCTCACGCAGCCAGCGGACACTGTCAACTGACGCAGCACCCCCAGCCAGGGCTGCCAC
 CCAGGCATACAGCCTAGTGGGCCAGAGGTGAGAGGTTCTGAACCAAAGAAAGTCCACCATG
 CTAATCTGACCAAAGCAGAAACCACACCCAGCATGATCCCCAGCCAGAGCAGGCCCTCCAA
 ACGGTCTGAATTACAATGGACTTGACTCCCACGCTTCTAGGAGTCAGGGCTTGGACTC
 TTCTCGTCATTGGAGCTCAAGTCACCAGCCACACAACCAGATGAGAGGTCATCTAAGTAGCA
 GTGAGCATTGACCGAACAGATTGAGCATTTCCTTACATACCAAAAGCAA
 AGGATGTAAGCTGATTGATCTGAAAAGGCATCTTATTGTCCTTAGACCAAGAGTAAGGG
 AAAGCAGGAGTCCAAATCTATTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGAAAGGTG
 AGGTGAATATACCTAAAACCTTTAATGTGGATATTGTTGATCAGTGCTTGATTACAATT
 TTCAAGAGGAATGGATGCTGTTGTAATTCTATGCAATTCTGCAAACATTATTGGATT
 ATTGTTATTGAGACAGTCAGCAGAACCCACAGCCTATTACACCTGCTACACCATGTAC
 TGAGCTAACCACTCTAACGAAACTCCAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC
 TTCATTGTCATAAGGTTGGATATTAATTCAAGGGAGTTGAAATAGTGGAGATGGAGA
 AGAGTGAATGAGTTCTCCACTCTAACGAAACTCTGACAAAGGATTGTGAAGAGCTTCCATCTGATGTT
 ATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTGTGGATTCCCTCAAAT
 CAGATGCCTCTAACGGACTTCTGCTAGATATTCTGGAAGGAGAAAATACAACATGTCAATT
 TATCAACGTCCTTAGAAAGAATTCTCTAGAGAAAAGGGATCTAGGAATGCTGAAAGATTA
 CCCAACATACCAATTATAGTCTCTTCTGAGAAAATGTGAAACCAGAAATTGCAAGACTGG
 GTGGACTAGAAAGGGAGATTAGATCAGTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA
 TGGTGCCAGGCACCTGAGGAAAATCCAGCAGGTGGAGGTTGCACTGAGCCGAGATTATGCC
 ATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

FIGURE 316

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419
><subunit 1 of 1, 373 aa, 1 stop
><MW: 41281, pI: 8.33, NX(S/T): 3
MSLLLLLVSYYVGTGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLTDNEGNQKV
VITYSSRHVYNNLTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
ILKVLVRPSKPCELEGELEGSDLTQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLTMYSGLYQCTAGNEAGKESCVRVTQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKDKEYEEEERPNEIREDAEAPKARLVKPSSSSGSRSSRGSSSTRSTANS
ASRSQRTLSTDAAQPGLATQAYSLVGPEVRGSEPKVHHANLTKAETTPSMIPSQSRAFQTV
```

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

FIGURE 317

CGCGAGGCGCGGGGAGCCTGGGACCAGGAGCGAGAGCCGCCTACCTGCAGCCGCCACGGCACGGCAGCCA
 CC**ATG**GCCTCCTGCTGTGCTTCGTCTGTGCGGAGTAGTGGATTTCGCCAGAAGTTGAGTATCACTACT
 CCTGAAGAGATGATTGAAAAAGCAAAGGGAAACTGCCTATGCCATGCAAATTACGCTTAGTCCCAGAAGA
 CCAGGGACCGCTGGACATCGAGTGGCTGATATCACCAGCTGATAATCAGAAGGGATCAAGTGATTATTTAT
 ATTCTGGAGACAAAATTATGACTACTATCCAGATCTGAAAGGCCAGTACATTACAGTAATGATCTC
 AAATCTGGTGTGATGCAATAATGTAACGAATTACAACGTGTCAGATATTGCCACATATCAGTGCAAAGTGAA
 AAAAGCTCTGGTGTGCAAATAAGAAGATTCATCTGGTAGTTCTGTTAACGCCCTCAGGTGCGAGATGTTACG
 TTGATGGATCTGAAGAAATTGGAAGTGCACCTTAAGATAAAATGTGAACCAAAAAGAAGGTTCACTCCATTACAG
 TATGAGTGCACAGAAAATTGTCGACTCACAGAAAATGCCCACTTACAGTTAGCAGAAAATGACTCATCTGTTAT
 ATCTGTAACAAAATGCCCTTCTGAGTACTCTGGACATACAGCTGACAGTCAGAAACAGAGTGGGCTCTGATC
 AGTGCCTGTTGCGTCTAACGTTGTCCTCCTTAACAAAGCTGGACTTAAGCTGAGGCCATTATAGGAAC
 TTGCTTGCCTAGCGCTCATTGGTCTTATCATCTTGCTGCTGCTAAAAGCGCAGAGAAGAAAATATGAAAA
 GGAAGTTCATCAGCATACAGGAAAGATGTGCCACCTCCAAAGAGCCGTACGTCCACTGCCAGAACGCTACATCG
 GCAGTAATCATTCCCTGGGTCCATGTCCTTCAACATGGAAGGATATTCAAGACTCAGTATAACCAA
 GTACCAAGTGAAGACTTTGAACGCACTCCTCAGAGTCCGACTCTCCACCTGCTAAGTCAAGTACCCCTACAA
 GACTGATGAAATTACAGTTGTA**TAA**ATATGGACTACTGAAGAATCTGAAGTATTGATTATTGACTTTATTT
 AGGCCTCTAGTAAAGACTTAAATGTTTAAAGCACAAGGCACAGAGATTAGAGCAGCTGTAAGAACAC
 ATCTACTTTATGCAATGGCATTAGACATGTAAGTCAGATGTCATGTCACAAATTAGTACGAGCCAATTCTTGT
 TAAAAAACCTATGTATAGTGCACACTGATAGTTAAAGATGTTTATTATATTTCAATAACTACCAACTAACAA
 ATTTTAACTTTCATATGCATATTCTGATATGTTCTTTAGGAAAAGTATGTTAATAGTTGATTTC
 AGGAAATTAAACCTTACGTTCTGTTAATGTTTGCTATTAGTTAAATACATTGAAGGAAATACCCG
 TTCTTCCCTTATGCACACAACAGAAACACGCGTTGTCATGCCCAAACATTGCAACTACA
 TGATTTCACACAATTCTCTTAAACACGACATAAAAGATTCTCTGTATATAAAACTACATACGCTCCA
 TAAAGTAATTCTCAAAGGTGCTAGAACAAATCGTCACCTCTACAGTGTCTCGTATCCAACAGAGTTGATGC
 ACAATATATAAAACTCAAGTCAATATTAAAACCTAGGCACCTGACTAACTTTAATAAAATTCTCAAACATA
 TATCAATATCTAAAGTCATATTAAAGAAAGATTATTCTCAATAACCTCTATAAAAATAAGTTGATGG
 TTTGCCCATCTAACTCACTATTAGTAAGAACCTTTAACTTTAATGTTGAGTAAAGGTTATTCTACCTT
 TTTCTCAACATGACACCAACAAATCAAACAGAAGTTAGTGAGGTGCTAACATGTGAGGATTAACTCCAGTGT
 TCCGGTCACATGCATTCCAGGAGGGTACCCATGTCACTGGAATTGGCGATATGTTTATTCTTCTGGCTT
 TGATTGGATAACCAAATGGAACAGGAGGGATAGTGTGATGGCCATTCCCTGATACATTCTGGCTT
 TTTCTGGGCAAAGGGTGCACATTGGAAAGGGTGGAAATATAAGTTCTGAAATCTGAGGGAAAGAACACAT
 TAAGTTAACTCAAAGGAAAAATCATCATCTATGTCAGGTCTAAATACATTAAAACCTCATGTGAAATAGGCGTATAA
 GAGATCACATCTAAGTGCACACTCCTATTGTCAGGTCTAAATACATTAAAACCTCATGTGAAATAGGCGTATAA
 TGTATAACAGGTGACCAATGTTCTGAATGCATAAAGAAATGAATAAAACTCAAACACAGTACTCCCTAAACAA
 CTTCAACCAAAAAGACCAAAACATGGAACGAATGGAAGCTTGTAGGACATGCTGTTTAGTCCAGTGGTT
 CCACAGCTGGCTAACGCCAGGAGTCACCTGGAGGCTTTAAATACAAAACATTGGAGCTGGAGGCCATTATCCT
 AGCAAACATAATGCAGAAACAGAAAATCAACTACCGCATGTTCTACCTTATAAGTGGAGGTAATGATAAGAACT
 TATGAACACAAAGAAGGAAACAATAGACATTGGAGTCTATTGAGAGGGAGGGTGGGAGAAGGAAAGGAGCA
 GAAAAGATAACTATTGAGTACTGCCTTCACACCTGGGTGATGAAATAATATGTACAACAAATCCCTGTGACACA
 TGTTTACCTATGGAACAAACCTCATGTGATCCCTAAACCTAAAGTTAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAA

FIGURE 318

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA82361
><subunit 1 of 1, 352 aa, 1 stop
><MW: 38938, pI: 7.86, NX(S/T): 3
MALLLCFVLLCGVVDFARSLSITTPEEMIEKAKGETAYLPCKFTLSPEDQGPLDIEWLISPA
DNQKVDQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVNLQLSDIGTYQCKVKK
APGVANKKIHLVVLVKPSGARCYVDGSEEIGSDFKIKCEPKEGSLPLQYEWQKLSDSQKMPT
SWLAEMTSSVISVKNASSEYSGTYSCTVRNRVGSDQCLLRNVVPPSNKAGLIAGAIIGTILL
ALALIGLIIIFCCRKKRREEKYEKEVHHDIREDVPPPRTSTARSYIGSNHSSLGSMSPSNM
EGYSKTQYNQVPSEDFERTPQSPTLPPAKFKYPYKTDGITVV
```

Signal sequence.

amino acids 1-19

Transmembrane domain:

amino acids 236-257

N-glycosylation sites.

amino acids 106-110, 201-205, 298-302

Tyrosine kinase phosphorylation sites.

amino acids 31-39, 78-85, 262-270

N-myristoylation sites.

amino acids 116-122, 208-214, 219-225, 237-243, 241-247,
245-251, 296-302

Myelin P0 protein.

amino acids 96-125

FIGURE 319

TGAAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCTATGCCTCTGATTGGTGA
 ATGGTGAAGGTGCCTGTCTAACCTTCCTGTAAAAAGAACCGAGCTGCCTCCAGGCAGCCAGCC
 CTCAAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTCGC
 CAATTTAACACCAAGAAGAATTGAGGCTGCTGGAGGAAGGCCAGGAGGAACACGAGACTG
 AGAGTGAATTTCAACAGAGGCTGCAAAGCCTGTGGACTTAGCCAGACCCTTGCCCTC
 CTTGCTGGCGACAGCCTCTCAAATGCAGATGGTTGTGCTCCCTGCCTGGGTTTACCTG
 CTTCTGGAGCCAGGTATCAGGGGCCAGGGCCAAGAATTCCACTTGGCCCTGCCAAGT
 GAAGGGGGTTGTTCCCCAGAAAATGTGGGAAGCCTCTGGCTGTGAAAGACACTATGCAAG
 CTCAGGATAACATCACGAGTGCCCGGCTGCTGCAGCAGGAGGTTCTGCAGAACGTCGGAT
 GCTGAGAGCTGTTACCTTGTCCACACCCCTGCTGGAGTTCTACTTGAAAATGTTTCAAAA
 CCACCACAATAGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTACTCTGCCAACAACT
 TTGTTCTCATCGTGTACAAC TGCAACCCAGTCAAGAAAATGAGATGTTTCCATCAGAGAC
 AGTGCACACAGGCAGGTTCTGCTATTCCGGAGAGCATTCAAACAGTTGGACGTAGAACGCAGC
 TCTGACCAAAGCCCTGGGAAGTGGACATTCTCTGACCTGGATGCAGAAATTCTACAAGC
 TCTGAATGTCTAGACCAGGACCTCCCTCCCCCTGGCACTGGTTGTTCCCTGTGTCATTCA
 AACAGTCTCCCTTCATGCTGTTCACTGGACACTTCACGCCCTGGCCATGGTCCCATT
 TTGGCCCAAGGATTATTGTCAAAGAACAGTCATTCTTAAGCAGGCCAGTGACAGTCAGGGAAG
 GTGCCTCTGGATGCTGTGAAGAGTCTACAGAGAACAGATTCTGTATTACAACTCTATT
 AATTAATGTCAGTATTCAACTGAAGATTCTATTATTGTGAGACTGTAAGTTACATGAAGG
 CAGCAGAATATTGTGCCCATGCTCTTACCCCTACAATCCTGCCACAGTGTGGGCAG
 TGGATGGGTGCTTAGTAAGTACTTAATAAAACTGTGGTGCTTTGGCCTGTCTTGGATT
 GTTAAAAAACAGAGAGGGATGCTGGATGTAAGACTGAACCTCAGAGCATGAAAATCACACT
 GTCTTCTGATATCTGCAGGGACAGAGCATTGGGTGGGGTAAGGTGCATCTGTTGAAAAG
 TAAACGATAAAATGTGGATTAAAGTGCCAGCACAAGCAGATCCTCAATAAACATTCAATT
 TCCCCACCAACTGCCAGCTCACCCATCATCCCTTCCCTGGTGCCCTCCTTTTT
 TATCCTAGTCATTCTCCCTAACATCTCCACTTGAGTGTCAAGCTGACCTGCTGATGGTGAC
 ATTGCACCTGGATGTACTATCCAATCTGTGATGACATTCCCTGCTAATAAAAGACAACATAA
 CTCCAAAAAAAAAAAAAAAAAAAAAA

320/330

FIGURE 320

>/usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002
>subunit 1 of 1, 206 aa, 1 stop
>**MW: 23799, pi: 9.12, NX(S/T): 3**
MNFQQRLQSLWTLARPFCPPLLATASQMQMVMVLPCLGFTLLLWSQVSGAQQGQEFGFGPCQVK
GVVPQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLVHTLLEFYLKTVFKNH
HNRTVEVRTLKSFSTLANNFVLIVSQLQPSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAAL
TKALGEVDILLTWMQKFYKL

Signal sequence:

amino acids 1-42

N-glycosylation sites.

amino acids 85-89, 99-103, 126-130

FIGURE 321

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGCATGAAGTTACAGTGTGTTCCCTTGGCTC
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTC
CACAGACATGCACCATATAGAAGAGAGTTCCAAGAAAATCAAAGAGCCATCCAAGCTAAGG
ACACCTCCCAAATGTCACTATCCTGTCCACATTGGAGACTCTGCAGATCATTAAGCCCTTA
GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTACGTGGACAGGGTGTCAAGGATCA
TCAGGAGCCAAACCCCCAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTCCTCTACA
TGCAGAAAACCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC
AATGCCACCAGAGTCATCCATGACAACATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
ATCCCTGGGAGAGCTCGACGTCTTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT
CAGCTTGATGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCCCTGTGCGGTTACT
GTGGGAGACAGCCCACCTGAAGGGGAAGGAGATGGGGAAAGGCCCTGCAGCTGAAAGTCC
CACTGGCTGGCCTCAGGCTGTCTATTCCGCTTGAAAATAGGCAAAAGTCTACTGTGGTAT
TTGTAATAAAACTCTATCTGCTGAAAGGCCCTGCAGGCCATCCTGGAGTAAAGGGCTGCCTT
CCCATCTAATTATTGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT
GTAGTACACATTGTACTGAGTGGTTTCTGAATAAATTCCATATTTACCTATGA

FIGURE 322

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282
><subunit 1 of 1, 177 aa, 1 stop
><MW: 20452, pI: 8.00, NX(S/T): 2
MKLQCVSLWLLGTILILCSVNDHGLRRCLISTDMHHIEESFQEIKRAIQAKDTFPNVTLST
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ
RQCHCRQEATNATRVIHDNYDQLEVHAAAIKSLGELDVFLAWINKHEVMFSA
```

Signal sequence:

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

FIGURE 323

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCACTGGCTCGTTAG
AACGCGCTACAATTAAACATAACCTTATGTATCATACACATACGATTAGGTGACACTAT
AGAATAACATCCACTTGCCTTCACAGGTGTCCACTCCCAGGTCCAACTCACCTC
GGTTCTATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCACG**ATG**TTGGGGCCCGCCT
CAGGCTCTGGTCTGTGCCTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCA
ATGCCTCCCCACTGCTCGGCTCCAGCTGGGTGGCCTGATCCACCTGTACACAGCCACAGCC
AGGAACAGCTACCACCTGCAGATCCACAAGAATGCCATGTGGATGGCGCACCCATCAGAC
CATCTACAGTGCCTGATGATCAGATCAGAGGATGCTGGTTGTGGTATTACAGGTGTGA
TGAGCAGAAGATACTCTGCATGGATTCAGAGGCAACATTTGGATCACACTATTCGAC
CCGGAGAACTGCAGGTTCAAACACCAAGACGCTGGAAAACGGTACGACGTCTACCACTCTCC
TCAGTATCACTCCTGGTCAGTCTGGCCGGCGAAGAGAGGCCTCCTGCCAGGCATGAACC
CACCCCCGTACTCCCAGTTCTGTCCGGAGGAACGAGATCCCCCTAATTCACTCAACACC
CCCATAACCACGGCGGCACACCCGGAGCGCCGAGGACACTGGAGCGGGACCCCTGAACGT
GCTGAAGCCCCGGGCCGGATGACCCGGCCCTCCTGTTACAGGAGCTCCGAGCG
CCGAGGACAACAGCCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGCGGTGAGTGAAC
ACGCACGCTGGGGAACGGGCCGGAAGGCTGCCGCCCTCGCCAAGTTCATC**TAG**GGTCG
CTGG

FIGURE 324

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142238
><subunit 1 of 1, 251 aa, 1 stop
><MW: 27954, pI: 9.22, NX(S/T): 1
MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARN SYHLQIHKNGHVD
GAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENC RFQHQTL ENGY
DVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRNEIPLIHFNTPIP RRHTRSAEDDSE
RDPLNVLKPRARMTPAPASC SQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTGPEGCRPFA
KFI
```

Important features of the protein:

Signal peptide:

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 175-179

N-myristoylation site.

amino acids 33-39, 100-106, 225-231, 229-235

HBGF/FGF family proteins

amino acids 73-124

FIGURE 325

GGAAAAGGTACCCCGAGAGAGACAGCCAGCAGTTCTGGAGCAGCGGTGGCCGGCTAGGATG
 GGCTGTCTCTGGGTCTGGCTCTGCCCTTTCTTCTGCTGGAGGTTGGGTCTCTGG
 GAGCTCTGCAGGCCAGCACCCGAGAGCAGACACTGCGATGACAACGGACGACACAGAAG
 TGCCCCTATGACTCTAGCACCGGCCACGCCCTGGAAACTCAAACGCTGAGCGCTGAG
 ACCTCTTAGGGCCTCAACCCAGCCGGCCCCATTCCAGAAGCAGAGACCAGGGAGCAA
 GAGAATTCCCCTGCAAGAGAGACCAGGAGTTCACAAAAACATCTCCAACTTCATGGTGC
 TGATGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC
 ACAGTTCAGACCATCACAGGCAGTGATCCCGAGGAAGCCATTTGACACCCTTGACCGA
 TGACAGCTCTGAAGAGGCAAAGACACTCACAATGGACATATTGACATTGGCTCACACCTCCA
 CAGAACGTAAGGCCTGCTCAGAGAGCAGCGCCTTCCGACGGCCCCCATCCAGTCATCACCC
 ACCCGTCACGGCCTCAGAGAGCAGCGCCTTCCGACGGCCCCCATCCAGTCATCACCC
 GTCACGGCCTCAGAGAGCAGCGCCTTCCGACGGCCCCCATCCAGTCATCACCCGT
 GGTCCCCGGATCTGATGTCACTCTCCTCGCTGAAGCCCTGGTACTGTCACAAACATCGAG
 GTTATTAAATTGCAGCATCACAGAAATAGAAACAACACTCCAGCATCCCTGGGCCTCAGA
 CATAGATCTCATCCCCACGGAAGGGTGAAGGCCTCGCACCTCCGATCCACCAGCTCTGC
 CTGACTCCACTGAAGCAAACACACATCACTGAGGTACAGCCTCTGCCGAGACCCTGTCC
 ACAGCCGGCACACAGACTCAGTCACCTCATGCCACGGTGGGACCCACTCCCCACTAA
 CAGGCCACAGAAAGAGAAGTGAAGCAGCACCCGGGCCAGCACCTCAGGGAGCTCTGGTCA
 CAGTTAGCAGGAATCCCCTGGAAGAAACCTCAGCCCTCTGTTGAGACACCAAGTTACGTC
 AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGCTGGTCAGCAGTGGCAAAACAACCTC
 CTTGCTGGAGCTCTGCTTCCCTACAGCCCTCGGAAGCCGCCCCCTAAGAACCTCACCC
 CTTCAGAGACACCGACCATGGACATCGAACCAAGGGGCCCTCCCCACCAGCAGGGACCC
 CTTCTCTGTCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTAGCCAA
 GATCACAAACCTCAGCGAAGACCACGATGAAGCCCCAACAGCCACGCCACGACTGCCGGAC
 GAGGCCGACCACAGACGTGAGTGCAGGTGAAATGGAGGTTCCCTCCTGCGGCTGAGTG
 TGGCTTCCCCGGAAGACCTCACTGACCCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC
 CGGGAACTCCACGCCACGCGCCTCACTCCAGGTCTCCTACTGCGTGTCAAGGAGAGGCTA
 ACGGACATCAGCTGCAGCCAGGCATGTCCGTATGCCAAAAGAGGGTGTGCCCCTAGCCTG
 GGCCCCCACCAGACAGACTGCAGCTGCCTACTGTGCTGAGAGGTACCCAGAAGGTTCCATG
 AAGGGCAGCATGTCCAAGCCCTAACCCAGATGTGGCAACAGGACCCCTGCTCACATCCAC
 CGGAGTGTATGTATGGGGAGGGCTTCACCTGTTCCAGAGGTGTGCTGGACTCACCTGG
 CACATGTTCTGTGTTCAAGAGAGACCTGATCACCCATCTGTGTGCTTCCATCCTGCA
 TTAAAATTCACTCAGTGTGGCCAAAAAAA

FIGURE 326

MGCLWGLALPLFFCWEVGVSGSSAGPSTRRADTAMTTDDTEVPAMTLAPGHALETQTLSA
ETSSRASTPAGPIPEAETRGAKRISPARERSFTKTPNFMVLIATSVETSAASGSPEGAGM
TTVQTITGSDPEEAIFDTLCTDDSSEEAKTLTMDIILTLAHTSTEAKGLSSESSASSDGPHPV
ITPSRASESSASSSDGPHPVITPSRASESSASSDGPHPVITPSWSPGSDVTLLAEALVTVTNI
EVINCSITEIETTSSIPGASDIDLIPTEGVKASSTDPPALPDSTEAKPHITEVTASAETL
STAGTTESAAPHATVGTPLPTNSATEREVTAPGATTLSGALVTVSRNPLEETSALSVETPSY
VKVSGAAPVSIEAGSAVGKITSFAGSSASSYSPSEAALKNFTPSETPTMDIATKGPFPTS RD
PLPSVPPTTNSSRGTNSTLAKITTSAKTTMKPQQPRPRLPGRGRPQT

N-glycosylation sites:

amino acids 252-256, 445-449, 451-455

cAMP-and cGMP-dependent protein kinase phosphorylation site.

amino acids 84-90

Casein kinase II phosphorylation sites.

amino acids 37-41, 108-112, 131-135, 133-137, 148-152, 165-169,
246-250, 254-258, 256-260, 269-273, 283-287, 333-337, 335-339,
404-408, 414-418, 431-435

N-myristoylation sites.

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284, 314-
320, 349-355, 386-392, 397-403, 449-455

ATP/GTP-binding site motif A (P-loop).

amino acids 385-393

FIGURE 327

GCGGAGCATCCGCTCGGGCCTGCCGAGACCCCCGCGCGGATTGCCGGTCCTCCCGCGG
 GCGCGACAGAGCTGCCTCGCACCTGGATGGCAGCAGGGCGCCGGGTCTCGACGCCA
 GAGAGAAATCTCATCATCTGTGCAGCCTTAAAGCAAACTAAGACCAGAGGGAGGATTAT
 CCTTGACCTTGAAGACCAAAACTAAACTGAAATTAAA**ATG**TCTCGGGGGAGAAGGGAG
 CTTGACTTACACTTGGTAATAATTGCTTCTGACACTAAGGCTGTCTGCTAGTCAGAATT
 GCCTCAAAAAGAGTCTAGAACGATGTTGTCATTGACATCCAGTCATCTCTTCTAAGGGAATC
 AGAGGCAATGAGCCGTATATACTCAACTCAAGAACGACTGCATTAATTCTGCTGTTAAC
 AAAAAACATATCAGGGACAAAGCATGTAACCTGATGATCTCGACACTCGAAAAACAGCTA
 GACAACCCAACGTGCTACCTATTTCTGTCCAACGAGGAAGCCTGTCATTGAAACCAGCA
 AAAGGACTTATGAGTTACAGGATAATTACAGATTTCATCTTGCACAGAAATTGCCAAG
 CCAAGAGTTACCCCAGGAAGATTCTCTTACATGCCAATTTCACAAGCAGTCACCCCC
 TAGCCCACATCACACAGATTATTCAAAGCCCACCGATATCTCATGGAGAGACACACTTCT
 CAGAAGTTGGATCCTCAGATCACCTGGAGAAACTATTAAAGATGGATGAAGCAAGTGCCA
 GCTCCTGCTATAAGGAAAAGGCCATTCTCAGAGTTACAATTTCCTGATCAAGAAA
 TAGCTCATCTGCTGCCTGAAAATGTGAGTGCCTCCAGCTACGGTGGCAGTTGCTTCTCA
 CATAACCACCTCGGCTACTCCAAAGCCGCCACCCCTCTACCCACCAATGCTTCAGTGACACC
 TTCTGGGACTTCCCAGCCACAGCTGGCCACCAAGCTCCACCTGTAACCACTGTCACTTCTC
 AGCCTCCCACGACCCCTACAGTTTACACGGCTGGCTACACTCCAAGCAATG
 GCTACAACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA
 AACCATACCGTTACAGAAATCTCAACTTAACCTTGAACACAGGGAAATGTGTATAACCCTA
 CTGCACATTCTATGTCATGTGAACTGGAGTCTTCCACTATGAATAAAACTGCTTCTGGGAAGGT
 AGGGAGGCCAGTCCAGGCAGTTCTCCAGGGCAGTGTCCAGAAAATCAGTACGGCCTTCC
 ATTTGAAAAATGGCTCTTATCGGGTCCCTGCTTTGGTGTCTGTTGGTGTAGGCC
 TCGTCCTCCTGGGTAGAATCCTTCGGAATCACTCCGAGGAAACGTTACTCAAGACTGGAT
 TATTGATCAATGGATCTATGTGGACAT**TAA**GGATGGAACCTGGTGTCTTAATTCTT
 TAGTAACCAGAAGCCCAATGCAATGAGTTCTGCTGACTTGCTAGTCTTAGCAGGAGGTTG
 TATTGAAAGACAGGAAATGCCCTCTGCTTTCTTGTGTTGGTGTAGAGACAGAGTCTT
 GCTCTGTTGCCAGGCTGGAGTGCAGTAGCACGATCTGGCTCTCACCGAACCTCCGTCTC
 CTGGGTCAAGCGATTCTCCTGCCCTAGCCTCTAAGTATCTGGATTACAGGCATGTGCCA
 CCACACCTGGGTGATTTGTATTCTAGTAGAGACGGGGTTTCACCATGTTGGTCAGGCTG
 GTCTCAAACCTCTGACCTAGTGATCCACCCCTCGGCCTCCAAAGTGTGGATTACAGG
 CATGAGCCACCAAGCTGGCCCCCTCTGTTATGTTGGTTGGAGAAGGAATGAAGTG
 GGAACCAAATTAGGTAATTGGGTAACTGTCTCTAAATATTAGCTAAAACAAAGCTCT
 ATGTAAAGTAATAAAAGTATAATTGCCATATAAAATTCAAAACTGCTTGTGAAAC
 GAAACAGGTTAGGACATCTAGGTTCCAATTCACATTCTGGTTCCAGATAAAACTAAC
 TGTTATATCAATTCTAATGGATTGCTTTCTTTATATGGATTCCCTTAAACTTATT
 CCAGATGTAGTCCCTCCAATTAAATATTGAATAATCTTGTACTCAA

FIGURE 328

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
><subunit 1 of 1, 431 aa, 1 stop
><MW: 46810, pI: 6.45, NX(S/T): 6
MFFGGEGSLTYLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSL SKGIRGNEPVYTSTQED
CINS CCSTKNISGDKACNLMIFDTRKTARQPN CYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTSQPP TTLISTVFTRAA TLQAMATTAVLTTTFQAP
TDSKG SLETIPFTEISNLT LNTGNVYNPTALSMSNVESSTMNKTA SWEGREASPGSSSQGSV
PENQYGLPFEKWL LIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSR LDYILINGIYVDI
```

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

FIGURE 329

CTCCCACGGTGTCCAGCGCC CAGA**ATG** CGGCTCTGGCTCTGCATGGGTTGCCTGCTGCT
 CCCAGGTTATGAAGCCCTGGAGGGGCCAGAGGAAATCAGCGGGTCGAAGGGGACACTGTGT
 CCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGT
 GGGATCCTCTCTCGCTCTGGCACCATCTATGCAGAAGAAGAAGGCCAGGAGAACAT
 GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTATTGTGACCCCTGTGGA
 ACCTCACCTGCAAGACGCTGGGGAGTACTGGTGTGGGTGAAAAACGGGGCCCCGATGAG
 TCTTACTGATCTCTGTGCTTCCAGGACCTGCTGTCCTCCCTCCAC
 CTTCCAGCCTCTGGCTACAACACGCCGCAGGCCAAGGCAAAGCTCAGCAAACCCAGGCC
 CAGGATTGACTTCTCCTGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGAAAGACAGGG
 GCTGAGGCCCTCCATTGCCAGGGACTTCCCAGTACGGGCACGAAAGGACTTCTCAGTACAC
 AGGAACCTCTCCTCACCCAGCGACCTCTCCTGCAGGGAGCTCCGCCCTCCATGCAGC
 TGGACTCCACCTCAGCAGAGGACACCAGTCCAGCTCAGCAGTGGCAGCTAAGCCCAGG
 GTGTCCATCCCGATGGTCCCGCATACTGGCCCCAGTCTGGTGTGCTGAGCCTCTGTGAGC
 CGCAGGCCTGATGCCCTCTGCAGCCACCTGCTCCTGTGGAGAAAGGAAGCTAACAGGCCA
 CGGAGACACAGAGGAACGAGAAGTCTGGCTCTCACGCTTGACTGCCAGGAAAAGGAAGCC
 CCTTCCCAGGCCCTGAGGGGGACGTGATCTCGATGCCCTCCACACATCTGAGGAGGA
 GCTGGCTCTCGAAGTTGTCTCAGCG**TAC** GGCAGGAGGCCCTCTGCCAGGCCAGCAGT
 GAAGCAGTATGGCTGGATCAGCACCGATTCCGAAAGCTTCCACCTCAGCCTCAGAG
 TCCAGCTGCCGGACTCCAGGGCTCTCCACCCCTCCCCAGGCTCTCCTCTGCATGTTCCA
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 GAGACTGGGACATCCCTGATAGGTTCACATCCCTGGCAGAGTACCAAGGCTGTCACCCTCA
 GCAGGGCCAGACAAGGCTCAGTGGATCTGGCTGAGTTCAATCTGCCAGGAACCTCTGGC
 CTCATGCCAGTGTGGACCCCTGCCCTCCACTCCAGACCCCACCTGTCTCCCTC
 TGGCGTCTCAGACTTAGTCCCACGGTCTCCTGCATCAGCTGGTGTGAAAGAGGAGCATGCT
 GGGGTGAGACTGGATTCTGGCTCTCTTGAACCACCTGCATCCAGCCTTCAGGAAGCCT
 GTGAAAAACGTGATTCTGGCCCCACCAAGACCCACCAAAACCATCTCTGGCTTGGTGCAG
 GACTCTGAATTCTAACATGCCAGTGAATGTCGCACTTGAGTTGAGGGCCAGTGGCCTG
 ATGAACGCTCACACCCCTCAGCTTAGAGTCTGCATTGGCTGTGACGTCTCACCTGCC
 CAATAGATCTGCTCTGTCGACACCAGATCCACGTGGGACTCCCTGAGGCCTGCTAAG
 TCCAGGCCCTGGTCAGGTCAAGGTGACATTGCAGGATAAGCCAGGACGGCACAGAAGTGG
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 AACCTTGGCTCCTCTGTCTGAAAGGGTTACTTGCTATGGTTCTGGTGGCTAGAGA
 GAAAAGTAGAAAACCAGAGTGCACGTAGGTGTAACACAGAGGAGAGTAGGAACAGGGCGG
 ATACCTGAAGGTGACTCCGAGTCCAGCCCTGGAGAAGGGTGGGGGTGGTAAAGTA
 GCACAACACTATTTTTCTTTCCATTATTATTGTTTTAAGACAGAACATCTCGTGCT
 GCTGCCAGGCTGGAGTGCAGTGGCACGATGCAAACCTCCGCCCTCTGGTTCAAGTGATT
 CTTCTGCCCTAGCCTCCCGAGTAGCTGGATTACAGGCACGCACCACACCTGGCTAATT
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 TTTACAGAGCAATTATCTGTATACAACTTGTATCCTGCCCTTCCACCTTATCGTTCC
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330/330

FIGURE 330

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GTIYAAEEGQETMKGRVSIRDSRQELSIVTLWNLTLDAGEYWCGVEKRGPDESLLISLFV
FPGPCCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGAEAPPLPG
TSQYGHERTSQYTGTSPHPATSPAGSSRPPMQLDSTAEDTSPALSSGSSKPRVSIPMVRI
LAPVLVLLSLLSAAGLIAFCSHLLWRKEAQATETQRNEKFWLRLTAEEKEAPSQAPEGD
VISMPPLHTSEEELGFSKFVSA
```

Important features:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128